

<110> Edwin L. Madison  
Edgar O. Ong  
Jiunn-Chern Yeh  
Corvas International, Inc.

<130> 24745-1607

<140> 09/000,000

<141> 2001-02-01

<150> 60/213,124

<151> 2000-06-22

<150> 60/234,840

<151> 2000-06-22

<150> 60/179,982

<151> 2000-02-03

<150> 60/183,542

<151> 2000-02-18

<150> 09/657,968

<151> 2000-02-08

<160> 72

<170> FastSEQ for Windows Version 4.0

<210> 1

$\langle 211 \rangle$  3147

<212> DNA

<213> Homo Sapien

 $\langle 220 \rangle$ 

<223> Nucleotide encoding MTSP1

<221> CDS

<222> (23) . . . (2589)

<300>

<301> O'Brien, T.J. and Tanimoto, H.

<308> GenBank AR081724

<310> US Pat 5972616

<311> 1998-02-20

<312> 1999-10-26

<400> 1

tcaagagcgg cctcggggta cc atg ggg agc gat cgg gcc cgc aag ggc gga 52  
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly  
1 5 10

ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cgg cac      100  
Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His

15                  20                  25

gag	aaa	gtg	aat	ggc	ttg	gag	gaa	ggc	gtg	gag	ttc	ctg	cca	gtc	aac	148
Glu	Lys	Val	Asn	Gly	Leu	Glu	Glu	Gly	Val	Glu	Phe	Leu	Pro	Val	Asn	
			30					35					40			
aac	gtc	aag	aag	gtg	gaa	aag	cat	ggc	ccg	ggg	cgc	tgg	gtg	gtg	ctg	196
Asn	Val	Lys	Lys	Val	Glu	Lys	His	Gly	Pro	Gly	Arg	Trp	Val	Val	Leu	
		45					50					55				
gca	gcc	gtg	ctg	atc	ggc	ctc	ctc	ttg	gtc	ttg	ctg	ggg	atc	ggc	ttc	244
Ala	Ala	Val	Leu	Ile	Gly	Leu	Leu	Leu	Val	Leu		Gly	Ile	Gly	Phe	
	60					65					70					
ctg	gtg	tgg	cat	ttg	cag	tac	cgg	gac	gtg	cgt	gtc	cag	aag	gtc	ttc	292
Leu	Val	Trp	His	Leu	Gln	Tyr	Arg	Asp	Val	Arg	Val	Gln	Lys	Val	Phe	
	75				80					85					90	
aat	ggc	tac	atg	agg	atc	aca	aat	gag	aat	ttt	gtg	gat	gcc	tac	gag	340
Asn	Gly	Tyr	Met	Arg	Ile	Thr	Asn	Glu	Asn	Phe	Val	Asp	Ala	Tyr	Glu	
				95					100					105		
aac	tcc	aac	tcc	act	gag	ttt	gta	agc	ctg	gcc	agc	aag	gtg	aag	gac	388
Asn	Ser	Asn	Ser	Thr	Glu	Phe	Val	Ser	Leu	Ala	Ser	Lys	Val	Lys	Asp	
			110					115					120			
gcg	ctg	aag	ctg	ctg	tac	agc	gga	gtc	cca	ttc	ctg	ggc	ccc	tac	cac	436
Ala	Leu	Lys	Leu	Leu	Tyr	Ser	Gly	Val	Pro	Phe	Leu	Gly	Pro	Tyr	His	
		125					130					135				
aag	gag	tcg	gct	gtg	acg	gcc	ttc	agc	gag	ggc	agc	gtc	atc	gcc	tac	484
Lys	Glu	Ser	Ala	Val	Thr	Ala	Phe	Ser	Glu	Gly	Ser	Val	Ile	Ala	Tyr	
	140					145					150					
tac	tgg	tct	gag	ttc	agc	atc	ccg	cag	cac	ctg	gtg	gag	gag	gcc	gag	532
Tyr	Trp	Ser	Glu	Phe	Ser	Ile	Pro	Gln	His	Leu	Val	Glu	Glu	Ala	Glu	
	155				160					165					170	
cgc	gtc	atg	gcc	gag	gag	cgc	gta	gtc	atg	ctg	ccc	ccg	cgg	gcg	cgc	580
Arg	Val	Met	Ala	Glu	Glu	Arg	Val	Val	Met	Leu	Pro	Pro	Arg	Ala	Arg	
				175					180					185		
tcc	ctg	aag	tcc	ttt	gtg	gtc	acc	tca	gtg	gtg	gct	ttc	ccc	acg	gac	628
Ser	Leu	Lys	Ser	Phe	Val	Val	Thr	Ser	Val	Val	Ala	Phe	Pro	Thr	Asp	
			190					195					200			
tcc	aaa	aca	gta	cag	agg	acc	cag	gac	aac	agc	tgc	agc	ttt	ggc	ctg	676
Ser	Lys	Thr	Val	Gln	Arg	Thr	Gln	Asp	Asn	Ser	Cys	Ser	Phe	Gly	Leu	
		205					210					215				
cac	gcc	cgc	ggt	gtg	gag	ctg	atg	cgc	ttc	acc	acg	ccc	ggc	ttc	cct	724
His	Ala	Arg	Gly	Val	Glu	Leu	Met	Arg	Phe	Thr	Thr	Pro	Gly	Phe	Pro	
	220					225					230					
gac	agc	ccc	tac	ccc	gct	cat	gcc	cgc	tgc	cag	tgg	gcc	ctg	cgg	ggg	772
Asp	Ser	Pro	Tyr	Pro	Ala	His	Ala	Arg	Cys	Gln	Trp	Ala	Leu	Arg	Gly	
	235				240				245					250		
gac	gcc	gac	tca	gtg	ctg	agc	ctc	acc	ttc	cgc	agc	ttt	gac	ctt	gcg	820
Asp	Ala	Asp	Ser	Val	Leu	Ser	Leu	Thr	Phe	Arg	Ser	Phe	Asp	Leu	Ala	
				255					260					265		
tcc	tgc	gac	gag	cgc	ggc	agc	gac	ctg	gtg	acg	gtg	tac	aac	acc	ctg	868
Ser	Cys	Asp	Glu	Arg	Gly	Ser	Asp	Leu	Val	Thr	Val	Tyr	Asn	Thr	Leu	

270					275					280						
agc	ccc	atg	gag	ccc	cac	gcc	ctg	gtg	cag	ttg	tgt	ggc	acc	tac	cct	916
Ser	Pro	Met	Glu	Pro	His	Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro	
		285					290					295				
ccc	tcc	tac	aac	ctg	acc	ttc	cac	tcc	tcc	cag	aac	gtc	ctg	ctc	atc	964
Pro	Ser	Tyr	Asn	Leu	Thr	Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile	
	300					305					310					
aca	ctg	ata	acc	aac	act	gag	cgg	cgg	cat	ccc	ggc	ttt	gag	gcc	acc	1012
Thr	Leu	Ile	Thr	Asn	Thr	Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	
315					320					325					330	
ttc	ttc	cag	ctg	cct	agg	atg	agc	agc	tgt	gga	ggc	cgc	tta	cgt	aaa	1060
Phe	Phe	Gln	Leu	Pro	Arg	Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	
				335					340					345		
gcc	cag	ggg	aca	ttc	aac	agc	ccc	tac	tac	cca	ggc	cac	tac	cca	ccc	1108
Ala	Gln	Gly	Thr	Phe	Asn	Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	
			350					355					360			
aac	att	gac	tgc	aca	tgg	aac	att	gag	gtg	ccc	aac	aac	cag	cat	gtg	1156
Asn	Ile	Asp	Cys	Thr	Trp	Asn	Ile	Glu	Val	Pro	Asn	Asn	Gln	His	Val	
		365					370					375				
aag	gtg	agc	ttc	aaa	ttc	ttc	tac	ctg	ctg	gag	ccc	ggc	gtg	cct	gcg	1204
Lys	Val	Ser	Phe	Lys	Phe	Phe	Tyr	Leu	Leu	Glu	Pro	Gly	Val	Pro	Ala	
	380					385					390					
ggc	acc	tgc	ccc	aag	gac	tac	gtg	gag	atc	aat	ggg	gag	aaa	tac	tgc	1252
Gly	Thr	Cys	Pro	Lys	Asp	Tyr	Val	Glu	Ile	Asn	Gly	Glu	Lys	Tyr	Cys	
395				400						405					410	
gga	gag	agg	tcc	cag	ttc	gtc	gtc	acc	agc	aac	agc	aac	aag	atc	aca	1300
Gly	Glu	Arg	Ser	Gln	Phe	Val	Val	Thr	Ser	Asn	Ser	Asn	Lys	Ile	Thr	
				415				420						425		
gtt	cgc	ttc	cac	tca	gat	cag	tcc	tac	acc	gac	acc	ggc	ttc	tta	gct	1348
Val	Arg	Phe	His	Ser	Asp	Gln	Ser	Tyr	Thr	Asp	Thr	Gly	Phe	Leu	Ala	
			430					435					440			
gaa	tac	ctc	tcc	tac	gac	tcc	agt	gac	cca	tgc	ccg	ggg	cag	ttc	acg	1396
Glu	Tyr	Leu	Ser	Tyr	Asp	Ser	Ser	Asp	Pro	Cys	Pro	Gly	Gln	Phe	Thr	
		445					450					455				
tgc	cgc	acg	ggg	cgg	tgt	atc	cgg	aag	gag	ctg	cgc	tgt	gat	ggc	tgg	1444
Cys	Arg	Thr	Gly	Arg	Cys	Ile	Arg	Lys	Glu	Leu	Arg	Cys	Asp	Gly	Trp	
	460					465					470					
gcc	gac	tgc	acc	gac	cac	agc	gat	gag	ctc	aac	tgc	agt	tgc	gac	gcc	1492
Ala	Asp	Cys	Thr	Asp	His	Ser	Asp	Glu	Leu	Asn	Cys	Ser	Cys	Asp	Ala	
475					480					485					490	
ggc	cac	cag	ttc	acg	tgc	aag	aac	aag	ttc	tgc	aag	ccc	ctc	ttc	tgg	1540
Gly	His	Gln	Phe	Thr	Cys	Lys	Asn	Lys	Phe	Cys	Lys	Pro	Leu	Phe	Trp	
				495				500						505		
gtc	tgc	gac	agt	gtg	aac	gac	tgc	gga	gac	aac	agc	gac	gag	cag	ggg	1588
Val	Cys	Asp	Ser	Val	Asn	Asp	Cys	Gly	Asp	Asn	Ser	Asp	Glu	Gln	Gly	
			510					515					520			

tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu 525 530 535	1636
tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser 540 545 550	1684
gac gag gcc tcc tgc ccc aag gtg aac gtc gtc act tgt acc aaa cac Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His 555 560 565 570	1732
acc tac cgc tgc ctc aat ggg ctc tgc ttg agc aag ggc aac cct gag Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu 575 580 585	1780
tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys 590 595 600	1828
gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly 605 610 615	1876
acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala 620 625 630	1924
ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp 635 640 645 650	1972
ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr 655 660 665	2020
tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser 670 675 680	2068
cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile 685 690 695	2116
tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu 700 705 710	2164
ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile 715 720 725 730	2212
tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp 735 740 745	2260
gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile 750 755 760	2308
ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn	2356

765					770					775						
ctc	ctg	ccg	cag	cag	atc	acg	ccg	cgc	atg	atg	tgc	gtg	ggc	ttc	ctc	2404
Leu	Leu	Pro	Gln	Gln	Ile	Thr	Pro	Arg	Met	Met	Cys	Val	Gly	Phe	Leu	
	780					785					790					
agc	ggc	ggc	gtg	gac	tcc	tgc	cag	ggt	gat	tcc	ggg	gga	ccc	ctg	tcc	2452
Ser	Gly	Gly	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ser	
	795				800					805					810	
agc	gtg	gag	gcg	gat	ggg	cgg	atc	ttc	cag	gcc	ggt	gtg	gtg	agc	tgg	2500
Ser	Val	Glu	Ala	Asp	Gly	Arg	Ile	Phe	Gln	Ala	Gly	Val	Val	Ser	Trp	
				815					820						825	
gga	gac	ggc	tgc	gct	cag	agg	aac	aag	cca	ggc	gtg	tac	aca	agg	ctc	2548
Gly	Asp	Gly	Cys	Ala	Gln	Arg	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Leu	
			830					835							840	
cct	ctg	ttt	cgg	gac	tgg	atc	aaa	gag	aac	act	ggg	gta	ta	ggggccgggg		2599
Pro	Leu	Phe	Arg	Asp	Trp	Ile	Lys	Glu	Asn	Thr	Gly	Val				
		845					850					855				
ccacccaaat	gtgtacacct	gcggggccac	ccatcggtcca	ccccagtggtg	cacgcctgca											2659
ggctggagac	tggaccgctg	actgcaccag	cgcccccaga	acatacactg	tgaactcaat											2719
ctccagggtc	ccaaatctgc	ctagaaaacc	tctcgcttcc	tcagcctcca	aagtggagct											2779
gggaggtaga	aggggaggac	actggtggtt	ctactgaccc	aactgggggc	aaaggtttga											2839
agacacagcc	tccccgcca	gcccgaagct	gggcccaggc	gcgtttgtgt	atatctgcct											2899
ccccgtgtctg	taaggagcag	cgggaacgga	gcttcggagc	ctcctcagtg	aaggtggtgg											2959
ggctgcccga	tctgggctgt	ggggcccttg	ggccacgctc	ttgaggaagc	ccaggctcgg											3019
aggaccctgg	aaaacagacg	ggtctgagac	tgaaattgtt	ttaccagctc	ccagggtgga											3079
cttcagtggtg	tgtattttgtg	taaatgggta	aaacaattta	tttcttttta	aaaaaaaaaa											3139
aaaaaaaaaa																3147
<210>	2															
<211>	855															
<212>	PRT															
<213>	Homo Sapien															
<400>	2															
Met	Gly	Ser	Asp	Arg	Ala	Arg	Lys	Gly	Gly	Gly	Gly	Pro	Lys	Asp	Phe	
1				5					10					15		
Gly	Ala	Gly	Leu	Lys	Tyr	Asn	Ser	Arg	His	Glu	Lys	Val	Asn	Gly	Leu	
			20					25					30			
Glu	Glu	Gly	Val	Glu	Phe	Leu	Pro	Val	Asn	Asn	Val	Lys	Lys	Val	Glu	
			35				40					45				
Lys	His	Gly	Pro	Gly	Arg	Trp	Val	Val	Leu	Ala	Ala	Val	Leu	Ile	Gly	
	50					55					60					
Leu	Leu	Leu	Val	Leu	Leu	Gly	Ile	Gly	Phe	Leu	Val	Trp	His	Leu	Gln	
65				70						75					80	
Tyr	Arg	Asp	Val	Arg	Val	Gln	Lys	Val	Phe	Asn	Gly	Tyr	Met	Arg	Ile	
				85					90					95		
Thr	Asn	Glu	Asn	Phe	Val	Asp	Ala	Tyr	Glu	Asn	Ser	Asn	Ser	Thr	Glu	
			100					105					110			
Phe	Val	Ser	Leu	Ala	Ser	Lys	Val	Lys	Asp	Ala	Leu	Lys	Leu	Leu	Tyr	
			115				120					125				
Ser	Gly	Val	Pro	Phe	Leu	Gly	Pro	Tyr	His	Lys	Glu	Ser	Ala	Val	Thr	
	130					135					140					
Ala	Phe	Ser	Glu	Gly	Ser	Val	Ile	Ala	Tyr	Tyr	Trp	Ser	Glu	Phe	Ser	
145				150					155						160	
Ile	Pro	Gln	His	Leu	Val	Glu	Glu	Ala	Glu	Arg	Val	Met	Ala	Glu	Glu	
				165					170					175		
Arg	Val	Val	Met	Leu	Pro	Pro	Arg	Ala	Arg	Ser	Leu	Lys	Ser	Phe	Val	

Val	Thr	Ser	Val	Val	Ala	Phe	Pro	Thr	Asp	Ser	Lys	Thr	Val	Gln	Arg
		195					200					205			
Thr	Gln	Asp	Asn	Ser	Cys	Ser	Phe	Gly	Leu	His	Ala	Arg	Gly	Val	Glu
	210					215					220				
Leu	Met	Arg	Phe	Thr	Thr	Pro	Gly	Phe	Pro	Asp	Ser	Pro	Tyr	Pro	Ala
225					230					235					240
His	Ala	Arg	Cys	Gln	Trp	Ala	Leu	Arg	Gly	Asp	Ala	Asp	Ser	Val	Leu
				245					250					255	
Ser	Leu	Thr	Phe	Arg	Ser	Phe	Asp	Leu	Ala	Ser	Cys	Asp	Glu	Arg	Gly
			260					265					270		
Ser	Asp	Leu	Val	Thr	Val	Tyr	Asn	Thr	Leu	Ser	Pro	Met	Glu	Pro	His
		275					280					285			
Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro	Pro	Ser	Tyr	Asn	Leu	Thr
		290				295					300				
Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile	Thr	Leu	Ile	Thr	Asn	Thr
305					310					315					320
Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	Phe	Phe	Gln	Leu	Pro	Arg
				325					330					335	
Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	Ala	Gln	Gly	Thr	Phe	Asn
			340					345					350		
Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	Asn	Ile	Asp	Cys	Thr	Trp
		355					360					365			
Asn	Ile	Glu	Val	Pro	Asn	Asn	Gln	His	Val	Lys	Val	Ser	Phe	Lys	Phe
		370				375					380				
Phe	Tyr	Leu	Leu	Glu	Pro	Gly	Val	Pro	Ala	Gly	Thr	Cys	Pro	Lys	Asp
385					390					395					400
Tyr	Val	Glu	Ile	Asn	Gly	Glu	Lys	Tyr	Cys	Gly	Glu	Arg	Ser	Gln	Phe
				405					410					415	
Val	Val	Thr	Ser	Asn	Ser	Asn	Lys	Ile	Thr	Val	Arg	Phe	His	Ser	Asp
			420					425					430		
Gln	Ser	Tyr	Thr	Asp	Thr	Gly	Phe	Leu	Ala	Glu	Tyr	Leu	Ser	Tyr	Asp
		435					440					445			
Ser	Ser	Asp	Pro	Cys	Pro	Gly	Gln	Phe	Thr	Cys	Arg	Thr	Gly	Arg	Cys
		450				455					460				
Ile	Arg	Lys	Glu	Leu	Arg	Cys	Asp	Gly	Trp	Ala	Asp	Cys	Thr	Asp	His
465					470					475					480
Ser	Asp	Glu	Leu	Asn	Cys	Ser	Cys	Asp	Ala	Gly	His	Gln	Phe	Thr	Cys
				485					490					495	
Lys	Asn	Lys	Phe	Cys	Lys	Pro	Leu	Phe	Trp	Val	Cys	Asp	Ser	Val	Asn
			500					505					510		
Asp	Cys	Gly	Asp	Asn	Ser	Asp	Glu	Gln	Gly	Cys	Ser	Cys	Pro	Ala	Gln
		515					520					525			
Thr	Phe	Arg	Cys	Ser	Asn	Gly	Lys	Cys	Leu	Ser	Lys	Ser	Gln	Gln	Cys
		530				535					540				
Asn	Gly	Lys	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Ala	Ser	Cys	Pro
545					550					555					560
Lys	Val	Asn	Val	Val	Thr	Cys	Thr	Lys	His	Thr	Tyr	Arg	Cys	Leu	Asn
				565					570					575	
Gly	Leu	Cys	Leu	Ser	Lys	Gly	Asn	Pro	Glu	Cys	Asp	Gly	Lys	Glu	Asp
			580					585					590		
Cys	Ser	Asp	Gly	Ser	Asp	Glu	Lys	Asp	Cys	Asp	Cys	Gly	Leu	Arg	Ser
		595					600					605			
Phe	Thr	Arg	Gln	Ala	Arg	Val	Val	Gly	Gly	Thr	Asp	Ala	Asp	Glu	Gly
		610				615					620				
Glu	Trp	Pro	Trp	Gln	Val	Ser	Leu	His	Ala	Leu	Gly	Gln	Gly	His	Ile
625					630					635					640
Cys	Gly	Ala	Ser	Leu	Ile	Ser	Pro	Asn	Trp	Leu	Val	Ser	Ala	Ala	His
				645					650					655	
Cys	Tyr	Ile	Asp	Asp	Arg	Gly	Phe	Arg	Tyr	Ser	Asp	Pro	Thr	Gln	Trp
			660					665					670		
Thr	Ala	Phe	Leu	Gly	Leu	His	Asp	Gln	Ser	Gln	Arg	Ser	Ala	Pro	Gly

```

        675              680              685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690              695              700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
    705              710              715              720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
        725              730              735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
    740              745              750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
    755              760              765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770              775              780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
    785              790              795              800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
        805              810              815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
    820              825              830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
    835              840              845
Ile Lys Glu Asn Thr Gly Val
    850              855

```

<210> 3

<211> 2137

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (261)...(1574)

<223> DNA sequence encoding a transmembrane serine  
protease (MTSP3) protein

<400> 3

```

ccatcctaatacgcactcactatagggctcgagcggccgcccgggcagggtcagagagaggc60
agcagcttgctcagcggacagagatgctgggcgtgagggacaaaggcctgccctgcactc120
gggcctcctccagccagtgtgaccagggaattctgacctgctggccagccaggacctgt180
gtggggaggccctcctgctgccttgggggtgacaatctcagctccaggctaaggaggacc240
gggaggatcacagagccagcatgtttagcagatcctgacagtgatcaacctctg293
          Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu
            1              5              10

```

```

aac agc ctc gat gtc aaa ccc ctg cgc aaa ccc cgt atc ccc atg gag341
Asn Ser Leu Asp Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu
          15              20              25

```

```

acc ttc aga aag gtg ggg atc ccc atc atc ata gca cta ctg agc ctg389
Thr Phe Arg Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu
          30              35              40

```

```

gcg agt atc atc att gtg gtt gtc ctc atc aag gtg att ctg gat aaa437
Ala Ser Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys
          45              50              55

```

```

tac tac ttc ctc tgc ggg cag cct ctc cac ttc atc ccg agg aag cag485
Tyr Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
          60              65              70              75

```

```

ctg tgt gac gga gag ctg gac tgt ccc ttg ggg gag gac gag gag cac533
Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His

```

80										85					90					
tgt	gtc	aag	agc	ttc	ccc	gaa	ggg	cct	gca	gtg	gca	gtc	cgc	ctc	tcc	581				
Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	Leu	Ser					
			95					100					105							
aag	gac	cga	tcc	aca	ctg	cag	gtg	ctg	gac	tcg	gcc	aca	ggg	aac	tgg	629				
Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	Gly	Asn	Trp					
		110					115					120								
ttc	tct	gcc	tgt	ttc	gac	aac	ttc	aca	gaa	gct	ctc	gct	gag	aca	gcc	677				
Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	Ala	Glu	Thr	Ala					
	125					130					135									
tgt	agg	cag	atg	ggc	tac	agc	agc	aaa	ccc	acc	ttc	aga	gct	gtg	gag	725				
Cys	Arg	Gln	Met	Gly	Tyr	Ser	Ser	Lys	Pro	Thr	Phe	Arg	Ala	Val	Glu					
140					145					150					155					
att	ggc	cca	gac	cag	gat	ctg	gat	gtt	gtt	gaa	atc	aca	gaa	aac	agc	773				
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	Ser					
				160					165					170						
cag	gag	ctt	cgc	atg	cgg	aac	tca	agt	ggg	ccc	tgt	ctc	tca	ggc	tcc	821				
Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	Gly	Ser					
			175					180					185							
ctg	gtc	tcc	ctg	cac	tgt	ctt	gcc	tgt	ggg	aag	agc	ctg	aag	acc	ccc	869				
Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	Lys	Thr	Pro					
		190					195					200								
cgt	gtg	gtg	ggg	ggg	gag	gag	gcc	tct	gtg	gat	tct	tgg	cct	tgg	cag	917				
Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	Trp	Pro	Trp	Gln					
	205					210					215									
gtc	agc	atc	cag	tac	gac	ata	cag	cac	gtc	tgt	gga	ggg	agc	atc	ctg	965				
Val	Ser	Ile	Gln	Tyr	Asp	Ile	Gln	His	Val	Cys	Gly	Gly	Ser	Ile	Leu					
220					225					230					235					
gac	ccc	cac	tgg	gtc	ctc	acg	gca	gcc	cac	tgc	ttc	agg	aaa	cat	acc	1013				
Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Phe	Arg	Lys	His	Thr					
				240				245						250						
gat	gtg	ttc	aac	tgg	aag	gtg	cgg	gca	ggc	tca	gac	aaa	ctg	ggc	agc	1061				
Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	Gly	Ser	Asp	Lys	Leu	Gly	Ser					
			255					260					265							
ttc	cca	tcc	ctg	gct	gtg	gcc	aag	atc	atc	atc	att	gaa	ttc	aac	ccc	1109				
Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro					
		270					275					280								
atg	tac	ccc	aaa	gac	aac	gac	atc	gcc	ctc	atg	aag	ctg	cag	ttc	cca	1157				
Met	Tyr	Pro	Lys	Asp	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro					
	285					290					295									
ctc	act	ttc	tca	ggc	aca	gtc	agg	ctc	atc	tgt	ctg	ccc	ttc	ttt	gat	1205				
Leu	Thr	Phe	Ser	Gly	Thr	Val	Arg	Leu	Ile	Cys	Leu	Pro	Phe	Phe	Asp					
300					305					310					315					
gag	gag	ctc	act	cca	gcc	acc	cca	ctc	tgg	atc	att	gga	tgg	ggc	ttt	1253				
Glu	Glu	Leu	Thr	Pro	Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe					
				320					325					330						

acg aag cag aat gga ggg aag atg tct gac ata ctg ctg cag gcg tca 1301  
 Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser  
 335 340 345  
 gtc cag gtc att gac agc aca cgg tgc aat gca gac gat gcg tac cag 1349  
 Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln  
 350 355 360  
 ggg gaa gtc acc gag aag atg atg tgt gca ggc atc ccg gaa ggg ggt 1397  
 Gly Gln Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly  
 365 370 375  
 gtg gac acc tgc cag ggt gac agt ggt ggg ccc ctg atg tac caa tct 1445  
 Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser  
 380 385 390 395  
 gac cag tgg cat gtg gtg ggc atc gtt agc tgg ggc tat ggc tgc ggg 1493  
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly  
 400 405 410  
 ggc ccg agc acc cca gga gta tac acc aag gtc tca gcc tat ctc aac 1541  
 Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn  
 415 420 425  
 tgg atc tac aat gtc tgg aag gct gag ctg taa tgctgtgtgcc cctttgcagt 1594  
 Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu \*  
 430 435  
 gctggggagcc gcttccttcc tgccctgccc acctggggat cccccaaagt cagacacaga 1654  
 gcaagagtcc ccttggttac acccctctgc ccacagcctc agcatttctt ggagcagcaa 1714  
 agggcctcaa ttcctgtaag agaccctcgc agcccagagg cgcccagagg aagtcagcag 1774  
 ccctagctcg gccacacttg gtgctcccag catcccaggg agagacacag cccactgaac 1834  
 aaggtctcag ggggtattgct aagccaagaa ggaactttcc cacactactg aatggaagca 1894  
 ggctgtcttg taaaagccca gatcactgtg ggctggagag gagaaggaaa gggctctgcgc 1954  
 cagccctgtc cgtcttcacc catccccaag cctactagag caagaaacca gttgtaatat 2014  
 aaaatgcact gccctactgt tggtatgact accgttacct actgttgtca ttgttattac 2074  
 agctatggcc actattatta aagagctgtg taacaaaaaa aaaaaaaaaa aaaaaaaaaa 2134  
 aaa 2137

<210> 4  
 <211> 437  
 <212> PRT  
 <213> Homo Sapien

<400> 4  
 Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val  
 1 5 10 15  
 Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val  
 20 25 30  
 Gly Ile Pro Ile Ile Ile Ala Leu Ser Leu Ala Ser Ile Ile Ile  
 35 40 45  
 Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys  
 50 55 60  
 Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu  
 65 70 75 80  
 Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe  
 85 90 95  
 Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr  
 100 105 110  
 Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe  
 115 120 125  
 Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly

130 135 140  
 Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln  
 145 150 155 160  
 Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met  
 165 170 175  
 Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His  
 180 185 190  
 Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly  
 195 200 205  
 Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr  
 210 215 220  
 Asp Ile Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val  
 225 230 235 240  
 Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp  
 245 250 255  
 Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala  
 260 265 270  
 Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp  
 275 280 285  
 Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly  
 290 295 300  
 Thr Val Arg Leu Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro  
 305 310 315 320  
 Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly  
 325 330 335  
 Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp  
 340 345 350  
 Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu  
 355 360 365  
 Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln  
 370 375 380  
 Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val  
 385 390 395 400  
 Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro  
 405 410 415  
 Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr Asn Val  
 420 425 430  
 Trp Lys Ala Glu Leu  
 435

<210> 5  
 <211> 708  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> CDS  
 <222> (1)...(708)  
 <223> MTSP4 protease domain cDNA

<400> 5  
 att gtt ggt gga gct gtg tcc tcc gag ggt gag tgg cca tgg cag gcc 48  
 Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala  
 1 5 10 15  
 agc ctc cag gtt cgg ggt cga cac atc tgt ggg ggg gcc ctc atc gct 96  
 Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala  
 20 25 30  
 gac cgc tgg gtg ata aca gct gcc cac tgc ttc cag gag gac agc atg 144  
 Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met  
 35 40 45

gcc tcc acg gtg ctg tgg acc gtg ttc ctg ggc aag gtg tgg cag aac 192  
 Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn  
 50 55 60

tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg 240  
 Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu  
 65 70 75 80

cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg 288  
 His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu  
 85 90 95

cag ctc gac cac ccg gtg gtg cgc tcg gcc gcc gtg cgc ccc gtc tgc 336  
 Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys  
 100 105 110

ctg ccc gcg cgc tcc cac ttc ttc gag ccc ggc ctg cac tgc tgg att 384  
 Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile  
 115 120 125

acg ggc tgg ggc gcc ttg cgc gag ggc ggc ccc atc agc aac gct ctg 432  
 Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu  
 130 135 140

cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc 480  
 Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val  
 145 150 155 160

tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc gcc tac cgc aag 528  
 Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys  
 165 170 175

ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc 576  
 Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
 180 185 190

aag gca ctc agt ggc cgc tgg ttc ctg gcg ggc ctg gtc agc tgg ggc 624  
 Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly  
 195 200 205

ctg ggc tgt ggc cgg cct aac tac ttc ggc gtc tac acc cgc atc aca 672  
 Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr  
 210 215 220

ggt gtg atc agc tgg atc cag caa gtg gtg acc tga 708  
 Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr \*  
 225 230 235

<210> 6  
 <211> 235  
 <212> PRT  
 <213> Homo Sapien

<400> 6  
 Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala  
 1 5 10 15  
 Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala  
 20 25 30  
 Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met  
 35 40 45

Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn  
 50 55 60  
 Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu  
 65 70 75 80  
 His Pro Tyr His Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu  
 85 90 95  
 Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys  
 100 105 110  
 Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile  
 115 120 125  
 Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu  
 130 135 140  
 Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val  
 145 150 155 160  
 Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys  
 165 170 175  
 Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
 180 185 190  
 Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly  
 195 200 205  
 Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr  
 210 215 220  
 Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr  
 225 230 235

&lt;210&gt; 7

&lt;211&gt; 3104

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (33)...(2441)

&lt;223&gt; cDNA encoding :MTSP4-L (long form) splice variant

&lt;400&gt; 7

tc	atc	ggg	cca	gag	ggg	tgatc	ag	atg	ccc	gtg	gcc	gag	gcc	ccc	53
								Met	Pro	Val	Ala	Glu	Ala	Pro	
								1				5			
cag	gtg	gct	ggc	ggg	cag	ggg	gac	gga	ggg	gat	ggc	gag	gaa	gcg	gag
Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu
			10				15					20			101
ccg	gag	ggg	atg	ttc	aag	gcc	tgt	gag	gac	tcc	aag	aga	aaa	gcc	cgg
Pro	Glu	Gly	Met	Phe	Lys	Ala	Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg
	25					30					35				149
ggc	tac	ctc	cgc	ctg	gtg	ccc	ctg	ttt	gtg	ctg	ctg	gcc	ctg	ctc	gtg
Gly	Tyr	Leu	Arg	Leu	Val	Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val
	40				45				50						55
ctg	gct	tcg	gcg	ggg	gtg	cta	ctc	tgg	tat	ttc	cta	ggg	tac	aag	gcg
Leu	Ala	Ser	Ala	Gly	Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala
				60					65					70	
gag	gtg	atg	gtc	agc	cag	gtg	tac	tca	ggc	agt	ctg	cgt	gta	ctc	aat
Glu	Val	Met	Val	Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn
			75					80					85		
cgc	cac	ttc	tcc	cag	gat	ctt	acc	cgc	cgg	gaa	tct	agt	gcc	ttc	cgc
Arg	His	Phe	Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg

	90		95		100	
	agt gaa acc gcc aaa gcc cag aag atg ctc aag gag ctc atc acc agc					389
	Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser					
	105		110		115	
	acc cgc ctg gga act tac tac aac tcc agc tcc gtc tat tcc ttt ggg					437
	Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly					
	120		125		130	135
	gag gga ccc ctc acc tgc ttc ttc tgg ttc att ctc caa atc ccc gag					485
	Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro Glu					
		140		145	150	
	cac cgc cgg ctg atg ctg agc ccc gag gtg gtg cag gca ctg ctg gtg					533
	His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu Leu Val					
		155		160	165	
	gag gag ctg ctg tcc aca gtc aac agc tcg gct gcc gtc ccc tac agg					581
	Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val Pro Tyr Arg					
		170		175	180	
	gcc gag tac gaa gtg gac ccc gag ggc cta gtg atc ctg gaa gcc agt					629
	Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile Leu Glu Ala Ser					
		185		190	195	
	gtg aaa gac ata gct gca ttg aat tcc acg ctg ggt tgt tac cgc tac					677
	Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu Gly Cys Tyr Arg Tyr					
		200	205		210	215
	agc tac gtg ggc cag ggc cag gtc ctc cgg ctg aag ggg cct gac cac					725
	Ser Tyr Val Gly Gln Gly Gln Val Leu Arg Leu Lys Gly Pro Asp His					
		220		225	230	
	ctg gcc tcc agc tgc ctg tgg cac ctg cag ggc ccc aag gac ctc atg					773
	Leu Ala Ser Ser Cys Leu Trp His Leu Gln Gly Pro Lys Asp Leu Met					
		235		240	245	
	ctc aaa ctc cgg ctg gag tgg acg ctg gca gag tgc cgg gac cga ctg					821
	Leu Lys Leu Arg Leu Glu Trp Thr Leu Ala Glu Cys Arg Asp Arg Leu					
		250		255	260	
	gcc atg tat gac gtg gcc ggg ccc ctg gag aag agg ctc atc acc tcg					869
	Ala Met Tyr Asp Val Ala Gly Pro Leu Glu Lys Arg Leu Ile Thr Ser					
		265	270		275	
	gtg tac ggc tgc agc cgc cag gag ccc gtg gtg gag gtt ctg gcg tcg					917
	Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val Leu Ala Ser					
		280	285		290	295
	ggg gcc atc atg gcg gtc gtc tgg aag aag ggc ctg cac agc tac tac					965
	Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr					
		300		305	310	
	gac ccc ttc gtg ctc tcc gtg cag ccg gtg gtc ttc cag gcc tgt gaa					1013
	Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu					
		315		320	325	
	gtg aac ctg acg ctg gac aac agg ctc gac tcc cag ggc gtc ctc agc					1061
	Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser					
		330	335		340	

acc ccg tac ttc ccc agc tac tac tcg ccc caa acc cac tgc tcc tgg	1109
Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp	
345 350 355	
cac ctc acg gtg ccc tct ctg gac tac ggc ttg gcc ctc tgg ttt gat	1157
His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp	
360 365 370 375	
gcc tat gca ctg agg agg cag aag tat gat ttg ccg tgc acc cag ggc	1205
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln Gly	
380 385 390	
cag tgg acg atc cag aac agg agg ctg tgt ggc ttg cgc atc ctg cag	1253
Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile Leu Gln	
395 400 405	
ccc tac gcc gag agg atc ccc gtg gtg gcc acg gcc ggg atc acc atc	1301
Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly Ile Thr Ile	
410 415 420	
aac ttc acc tcc cag atc tcc ctc acc ggg ccc ggt gtg cgg gtg cac	1349
Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly Val Arg Val His	
425 430 435	
tat ggc ttg tac aac cag tcg gac ccc tgc cct gga gag ttc ctc tgt	1397
Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro Gly Glu Phe Leu Cys	
440 445 450 455	
tct gtg aat gga ctc tgt gtc cct gcc tgt gat ggg gtc aag gac tgc	1445
Ser Val Asn Gly Leu Cys Val Pro Ala Cys Asp Gly Val Lys Asp Cys	
460 465 470	
ccc aac ggc ctg gat gag aga aac tgc gtt tgc aga gcc aca ttc cag	1493
Pro Asn Gly Leu Asp Glu Arg Asn Cys Val Cys Arg Ala Thr Phe Gln	
475 480 485	
tgc aaa gag gac agc aca tgc atc tca ctg ccc aag gtc tgt gat ggg	1541
Cys Lys Glu Asp Ser Thr Cys Ile Ser Leu Pro Lys Val Cys Asp Gly	
490 495 500	
cag cct gat tgt ctc aac ggc agc gac gaa gag cag tgc cag gaa ggg	1589
Gln Pro Asp Cys Leu Asn Gly Ser Asp Glu Glu Gln Cys Gln Glu Gly	
505 510 515	
gtg cca tgt ggg aca ttc acc ttc cag tgt gag gac cgg agc tgc gtg	1637
Val Pro Cys Gly Thr Phe Thr Phe Gln Cys Glu Asp Arg Ser Cys Val	
520 525 530 535	
aag aag ccc aac ccg cag tgt gat ggg cgg ccc gac tgc agg gac ggc	1685
Lys Lys Pro Asn Pro Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly	
540 545 550	
tcg gat gag gag cac tgt gaa tgt ggc ctc cag ggc ccc tcc agc cgc	1733
Ser Asp Glu Glu His Cys Glu Cys Gly Leu Gln Gly Pro Ser Ser Arg	
555 560 565	
att gtt ggt gga gct gtg tcc tcc gag ggt gag tgg cca tgg cag gcc	1781
Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala	
570 575 580	
agc ctc cag gtt cgg ggt cga cac atc tgt ggg ggg gcc ctc atc gct	1829
Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala	

585	590	595	
gac cgc tgg gtg ata aca gct gcc cac tgc ttc cag gag gac agc atg Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met 600 605 610 615			1877
gcc tcc acg gtg ctg tgg acc gtg ttc ctg ggc aag gtg tgg cag aac Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn 620 625 630			1925
tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu 635 640 645			1973
cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu 650 655 660			2021
cag ctc gac cac ccg gtg gtg cgc tcg gcc gcc gtg cgc ccc gtc tgc Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys 665 670 675			2069
ctg ccc gcg cgc tcc cac ttc ttc gag ccc ggc ctg cac tgc tgg att Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile 680 685 690 695			2117
acg ggc tgg ggc gcc ttg cgc gag ggc ggc ccc atc agc aac gct ctg Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu 700 705 710			2165
cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val 715 720 725			2213
tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc ggc tac cgc aag Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys 730 735 740			2261
ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys 745 750 755			2309
aag gca ctc agt ggc cgc tgg ttc ctg gcg ggg ctg gtc agc tgg ggc Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly 760 765 770 775			2357
ctg ggc tgt ggc cgg cct aac tac ttc ggc gtc tac acc cgc atc aca Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr 780 785 790			2405
ggg gtg atc agc tgg atc cag caa gtg gtg acc tga ggaactgccc Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr *			2451
cctgcaaag cagggccac ctctggact cagagagccc agggcaactg ccaagcaggg ggacaagtat tctggcgggg ggtgggggag agagcaggcc ctgtggtggc aggaggggca tctgttttcg tccctgatgt ctgtccagta tggcaggagg atgagaagtg ccagcagttg ggggtcaaga cgtcccttga ggaccacaggc ccacaccccag cccttttgcc tcccaattct ctctcctccg tccccttcct ccactgctgc ctaatgcaag gcagtggctc agcagcaaga atgctgggttc tacatcccga ggagtgtctg aggtgcgccc cactctgtac agaggctgtt tgggcagcct tgcctccaga gagcagattc cagcttcgga agcccctggt ctaacttggg atctgggaat ggaaggtgct cccatcggag gggaccctca gagccctgga gactgccagg			2511 2571 2631 2691 2751 2811 2871 2931

tgggcctgct gccactgtaa gccaaaaggt ggggaagtcc tgactccagg gtccttgccc 2991  
 caccctggcc tgccacctgg gccctcacag ccagaccct cactgggagg tgagctcagc 3051  
 tgccttttgg aataaagctg cctgatgcaa aaaaaaaaaa aaaaaaaaaa aaa 3104

<210> 8  
 <211> 802  
 <212> PRT  
 <213> Homo Sapien

<400> 8  
 Met Pro Val Ala Glu Ala Pro Gln Val Ala Gly Gly Gln Gly Asp Gly  
 1 5 10 15  
 Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala Cys Glu  
 20 25 30  
 Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val Pro Leu Phe  
 35 40 45  
 Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly Val Leu Leu Trp  
 50 55 60  
 Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val Ser Gln Val Tyr Ser  
 65 70 75 80  
 Gly Ser Leu Arg Val Leu Asn Arg His Phe Ser Gln Asp Leu Thr Arg  
 85 90 95  
 Arg Glu Ser Ser Ala Phe Arg Ser Glu Thr Ala Lys Ala Gln Lys Met  
 100 105 110  
 Leu Lys Glu Leu Ile Thr Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser  
 115 120 125  
 Ser Ser Val Tyr Ser Phe Gly Glu Gly Pro Leu Thr Cys Phe Phe Trp  
 130 135 140  
 Phe Ile Leu Gln Ile Pro Glu His Arg Arg Leu Met Leu Ser Pro Glu  
 145 150 155 160  
 Val Val Gln Ala Leu Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser  
 165 170 175  
 Ser Ala Ala Val Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly  
 180 185 190  
 Leu Val Ile Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser  
 195 200 205  
 Thr Leu Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu  
 210 215 220  
 Arg Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu  
 225 230 235 240  
 Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr Leu  
 245 250 255  
 Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly Pro Leu  
 260 265 270  
 Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg Gln Glu Pro  
 275 280 285  
 Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala Val Val Trp Lys  
 290 295 300  
 Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val Leu Ser Val Gln Pro  
 305 310 315 320  
 Val Val Phe Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asn Arg Leu  
 325 330 335  
 Asp Ser Gln Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser  
 340 345 350  
 Pro Gln Thr His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr  
 355 360 365  
 Gly Leu Ala Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr  
 370 375 380  
 Asp Leu Pro Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu  
 385 390 395 400  
 Cys Gly Leu Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val  
 405 410 415

Ala Thr Ala Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr  
 420 425 430  
 Gly Pro Gly Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro  
 435 440 445  
 Cys Pro Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala  
 450 455 460  
 Cys Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys  
 465 470 475 480  
 Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile Ser  
 485 490 495  
 Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly Ser Asp  
 500 505 510  
 Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe Thr Phe Gln  
 515 520 525  
 Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro Gln Cys Asp Gly  
 530 535 540  
 Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu His Cys Glu Cys Gly  
 545 550 555 560  
 Leu Gln Gly Pro Ser Ser Arg Ile Val Gly Gly Ala Val Ser Ser Glu  
 565 570 575  
 Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Val Arg Gly Arg His Ile  
 580 585 590  
 Cys Gly Gly Ala Leu Ile Ala Asp Arg Trp Val Ile Thr Ala Ala His  
 595 600 605  
 Cys Phe Gln Glu Asp Ser Met Ala Ser Thr Val Leu Trp Thr Val Phe  
 610 615 620  
 Leu Gly Lys Val Trp Gln Asn Ser Arg Trp Pro Gly Glu Val Ser Phe  
 625 630 635 640  
 Lys Val Ser Arg Leu Leu His Pro Tyr His Glu Glu Asp Ser His  
 645 650 655  
 Asp Tyr Asp Val Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser  
 660 665 670  
 Ala Ala Val Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu  
 675 680 685  
 Pro Gly Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly  
 690 695 700  
 Gly Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro  
 705 710 715 720  
 Gln Asp Leu Cys Ser Glu Val Tyr Arg Tyr Gln Val Thr Pro Arg Met  
 725 730 735  
 Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln Gly Asp  
 740 745 750  
 Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu  
 755 760 765  
 Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe  
 770 775 780  
 Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser Trp Ile Gln Gln Val  
 785 790 795 800  
 Val Thr

&lt;210&gt; 9

&lt;211&gt; 2672

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (33)...(2009)

&lt;223&gt; cDNA encoding: MTSP4-S (short form) splice variant

&lt;400&gt; 9

tcatacgcca gagggatgatc agtgagcaga ag atg ccc gtg gcc gag gcc ccc	53
Met Pro Val Ala Glu Ala Pro	
1 5	
cag gtg gct ggc ggg cag ggg gac gga ggt gat ggc gag gaa gcg gag	101
Gln Val Ala Gly Gly Gln Gly Asp Gly Gly Asp Gly Glu Glu Ala Glu	
10 15 20	
ccg gag ggg atg ttc aag gcc tgt gag gac tcc aag aga aaa gcc cgg	149
Pro Glu Gly Met Phe Lys Ala Cys Glu Asp Ser Lys Arg Lys Ala Arg	
25 30 35	
ggc tac ctc cgc ctg gtg ccc ctg ttt gtg ctg ctg gcc ctg ctc gtg	197
Gly Tyr Leu Arg Leu Val Pro Leu Phe Val Leu Leu Ala Leu Leu Val	
40 45 50 55	
ctg gct tcg gcg ggg gtg cta ctc tgg tat ttc cta ggg tac aag gcg	245
Leu Ala Ser Ala Gly Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala	
60 65 70	
gag gtg atg gtc agc cag gtg tac tca ggc agt ctg cgt gta ctc aat	293
Glu Val Met Val Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn	
75 80 85	
cgc cac ttc tcc cag gat ctt acc cgc cgg gaa tct agt gcc ttc cgc	341
Arg His Phe Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg	
90 95 100	
agt gaa acc gcc aaa gcc cag aag atg ctc aag gag ctc atc acc agc	389
Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser	
105 110 115	
acc cgc ctg gga act tac tac aac tcc agc tcc gtc tat tcc ttt ggg	437
Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly	
120 125 130 135	
gtg tac ggc tgc agc cgc cag gag ccc gtg gtg gag gtt ctg gcg tcg	485
Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val Leu Ala Ser	
140 145 150	
ggg gcc atc atg gcg gtc gtc tgg aag aag ggc ctg cac agc tac tac	533
Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr	
155 160 165	
gac ccc ttc gtg ctc tcc gtg cag ccg gtg gtc ttc cag gcc tgt gaa	581
Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu	
170 175 180	
gtg aac ctg acg ctg gac aac agg ctc gac tcc cag ggc gtc ctc agc	629
Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser	
185 190 195	
acc ccg tac ttc ccc agc tac tac tcg ccc caa acc cac tgc tcc tgg	677
Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp	
200 205 210 215	
cac ctc acg gtg ccc tct ctg gac tac ggc ttg gcc ctc tgg ttt gat	725
His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp	
220 225 230	
gcc tat gca ctg agg agg cag aag tat gat ttg ccg tgc acc cag ggc	773
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln Gly	

235										240					245					
cag	tgg	acg	atc	cag	aac	agg	agg	ctg	tgt	ggc	ttg	cgc	atc	ctg	cag	821				
Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile	Leu	Gln					
		250					255					260								
ccc	tac	gcc	gag	agg	atc	ccc	gtg	gtg	gcc	acg	gcc	ggg	atc	acc	atc	869				
Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly	Ile	Thr	Ile					
	265					270					275									
aac	ttc	acc	tcc	cag	atc	tcc	ctc	acc	ggg	ccc	ggg	gtg	cgg	gtg	cac	917				
Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly	Val	Arg	Val	His					
280					285					290					295					
tat	ggc	ttg	tac	aac	cag	tcg	gac	ccc	tgc	cct	gga	gag	ttc	ctc	tgt	965				
Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro	Gly	Glu	Phe	Leu	Cys					
				300					305					310						
tct	gtg	aat	gga	ctc	tgt	gtc	cct	gcc	tgt	gat	ggg	gtc	aag	gac	tgc	1013				
Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys	Asp	Gly	Val	Lys	Asp	Cys					
			315					320					325							
ccc	aac	ggc	ctg	gat	gag	aga	aac	tgc	gtt	tgc	aga	gcc	aca	ttc	cag	1061				
Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys	Val	Cys	Arg	Ala	Thr	Phe	Gln					
		330					335					340								
tgc	aaa	gag	gac	agc	aca	tgc	atc	tca	ctg	ccc	aag	gtc	tgt	gat	ggg	1109				
Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly					
	345					350					355									
cag	cct	gat	tgt	ctc	aac	ggc	agc	gac	gaa	gag	cag	tgc	cag	gaa	ggg	1157				
Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly					
360					365					370					375					
gtg	cca	tgt	ggg	aca	ttc	acc	ttc	cag	tgt	gag	gac	cgg	agc	tgc	gtg	1205				
Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val					
				380				385						390						
aag	aag	ccc	aac	cgg	cag	tgt	gat	ggg	cgg	ccc	gac	tgc	agg	gac	ggc	1253				
Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly					
			395					400					405							
tcg	gat	gag	gag	cac	tgt	gaa	tgt	ggc	ctc	cag	ggc	ccc	tcc	agc	cgc	1301				
Ser	Asp	Glu	Glu	His	Cys	Glu	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg					
		410				415						420								
att	gtt	ggg	gga	gct	gtg	tcc	tcc	gag	ggg	gag	tgg	cca	tgg	cag	gcc	1349				
Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala					
	425					430					435									
agc	ctc	cag	gtt	cgg	ggg	cga	cac	atc	tgt	ggg	ggg	gcc	ctc	atc	gct	1397				
Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala					
440					445					450					455					
gac	cgc	tgg	gtg	ata	aca	gct	gcc	cac	tgc	ttc	cag	gag	gac	agc	atg	1445				
Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met					
				460					465					470						
gcc	tcc	acg	gtg	ctg	tgg	acc	gtg	ttc	ctg	ggc	aag	gtg	tgg	cag	aac	1493				
Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val		Gln	Asn					
			475					480					485							

tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg 1541  
 Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu  
 490 495 500

cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg 1589  
 His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu  
 505 510 515

cag ctc gac cac ccg gtg gtg cgc tgc gcc gcc gtg cgc ccc gtc tgc 1637  
 Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys  
 520 525 530 535

ctg ccc gcg cgc tcc cac ttc ttc gag ccc ggc ctg cac tgc tgg att 1685  
 Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Ile  
 540 545 550

acg ggc tgg ggc gcc ttg cgc gag ggc ggc ccc atc agc aac gct ctg 1733  
 Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu  
 555 560 565

cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc 1781  
 Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val  
 570 575 580

tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc ggc tac cgc aag 1829  
 Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys  
 585 590 595

ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc 1877  
 Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
 600 605 610 615

aag gca ctc agt ggc cgc tgg ttc ctg gcg ggg ctg gtc agc tgg ggc 1925  
 Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly  
 620 625 630

ctg ggc tgt ggc cgg cct aac tac ttc ggc gtc tac acc cgc atc aca 1973  
 Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr  
 635 640 645

ggt gtg atc agc tgg atc cag caa gtg gtg acc tga ggaactgccc 2019  
 Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr \*  
 650 655

ccctgcaaag cagggccac ctccctggact cagagagccc agggcaactg ccaagcaggg 2079  
 ggacaagtat tctggcgggg ggtgggggag agagcaggcc ctgtggtggc aggaggggca 2139  
 tcttggtttcg tccctgatgt ctgtccagta tggcaggagg atgagaagtg ccagcagttg 2199  
 ggggtcaaga cgcccttga ggacccaggc ccacacccag cccttttgcc tcccaattct 2259  
 ctctcctccg tccccttcc cactgtctgc ctaatgcaag gcagtggctc agcagcaaga 2319  
 atgctgggttc tacatcccga ggagtgtctg aggtgcgccc cactctgtac agaggctgtt 2379  
 tgggcagcct tgccctcaga gagcagattc cagcttcgga agcccctggt ctaacttggg 2439  
 atctgggaat ggaagggtgct cccatcgagg gggaccccca gagccctgga gactgccagg 2499  
 tgggcctgct gccactgtaa gccaaaaggt ggggaagtcc tgactccagg gtccttgccc 2559  
 caccctgccc tgccacctgg gccctcacag ccagaccct cactgggagg tgagctcagg 2619  
 tgccctttgg aataaagctg cctgatgcaa aaaaaaaaaa aaaaaaaaaa aaa 2672

<210> 10  
 <211> 658  
 <212> PRT  
 <213> Homo Sapien  
 <400> 10

Met Pro Val Ala Glu Ala Pro Gln Val Ala Gly Gly Gln Gly Asp Gly  
 1 5 10 15  
 Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala Cys Glu  
 20 25 30  
 Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val Pro Leu Phe  
 35 40 45  
 Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly Val Leu Leu Trp  
 50 55 60  
 Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val Ser Gln Val Tyr Ser  
 65 70 75 80  
 Gly Ser Leu Arg Val Leu Asn Arg His Phe Ser Gln Asp Leu Thr Arg  
 85 90 95  
 Arg Glu Ser Ser Ala Phe Arg Ser Glu Thr Ala Lys Ala Gln Lys Met  
 100 105 110  
 Leu Lys Glu Leu Ile Thr Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser  
 115 120 125  
 Ser Ser Val Tyr Ser Phe Gly Val Tyr Gly Cys Ser Arg Gln Glu Pro  
 130 135 140  
 Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala Val Val Trp Lys  
 145 150 155 160  
 Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val Leu Ser Val Gln Pro  
 165 170 175  
 Val Val Phe Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asn Arg Leu  
 180 185 190  
 Asp Ser Gln Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser  
 195 200 205  
 Pro Gln Thr His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr  
 210 215 220  
 Gly Leu Ala Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr  
 225 230 235 240  
 Asp Leu Pro Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu  
 245 250 255  
 Cys Gly Leu Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val  
 260 265 270  
 Ala Thr Ala Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr  
 275 280 285  
 Gly Pro Gly Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro  
 290 295 300  
 Cys Pro Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala  
 305 310 315 320  
 Cys Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys  
 325 330 335  
 Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile Ser  
 340 345 350  
 Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly Ser Asp  
 355 360 365  
 Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe Thr Phe Gln  
 370 375 380  
 Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro Gln Cys Asp Gly  
 385 390 395 400  
 Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu His Cys Glu Cys Gly  
 405 410 415  
 Leu Gln Gly Pro Ser Ser Arg Ile Val Gly Gly Ala Val Ser Ser Glu  
 420 425 430  
 Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Val Arg Gly Arg His Ile  
 435 440 445  
 Cys Gly Gly Ala Leu Ile Ala Asp Arg Trp Val Ile Thr Ala Ala His  
 450 455 460  
 Cys Phe Gln Glu Asp Ser Met Ala Ser Thr Val Leu Trp Thr Val Phe  
 465 470 475 480  
 Leu Gly Lys Val Trp Gln Asn Ser Arg Trp Pro Gly Glu Val Ser Phe  
 485 490 495

Lys Val Ser Arg Leu Leu Leu His Pro Tyr His Glu Glu Asp Ser His  
                   500                  505                  510  
 Asp Tyr Asp Val Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser  
                   515                  520                  525  
 Ala Ala Val Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu  
                   530                  535                  540  
 Pro Gly Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly  
 545                  550                  555  
 Gly Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro  
                   565                  570                  575  
 Gln Asp Leu Cys Ser Glu Val Tyr Arg Tyr Gln Val Thr Pro Arg Met  
                   580                  585                  590  
 Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln Gly Asp  
                   595                  600                  605  
 Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu  
                   610                  615                  620  
 Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe  
 625                  630                  635  
 Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser Trp Ile Gln Gln Val  
                   645                  650                  655  
 Val Thr

<210> 11  
 <211> 1656  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> CDS  
 <222> (268)...(1629)  
 <223> DNA sequence encoding a transmembrane serine  
           protease (MTSP-6) protein

<400> 11  
 cgccccgggca ggtcagtaac actgtggcct actatctctt ccgtgggtgcc atctacattt 60  
 ttgggactcg ggaattatga ctgttttttg ttaatcgata ctgaatgcgc tttgtgtgga 120  
 ctgtcgaatt tcaaagattt accgtatgac caagatgcac ctgatgctac aagtataaat 180  
 aggggaacaa atgcttttctg ttcttccctcg gctaaggagg tagaggtgga ggcggagccg 240  
 gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt 294  
                                   Met Gly Glu Asn Asp Pro Pro Ala Val  
                                   1                                  5  
  
 gaa gcc ccc ttc tca ttc cga tgc ctt ttt ggc ctt gat gat ttg aaa 342  
 Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys  
   10                                  15                                  20                                  25  
  
 ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 390  
 Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu  
                                   30                                  35                                  40  
  
 tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att 438  
 Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile  
                                   45                                  50                                  55  
  
 gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc 486  
 Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys  
                   60                                  65                                  70  
  
 tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata 534  
 Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile  
   75                                  80                                  85

gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac	582
<b>Ala</b> Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	
90 95 100 105	
cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca	630
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr	
110 115 120	
gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac	678
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr	
125 130 135	
gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gta agt tca	726
Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser	
140 145 150	
gat aac ctc aga gtg agc tcg cta gag ggg cag ttc cgg gag gag ttt	774
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe	
155 160 165	
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac	822
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His	
170 175 180 185	
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc	870
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr	
190 195 200	
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc	918
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile	
205 210 215	
gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc	966
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser	
220 225 230	
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc	1014
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro	
235 240 245	
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc	1062
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr <b>Asp</b> Leu Tyr Leu Pro	
250 255 260 265	
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca	1110
Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro	
270 275 280	
gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag	1158
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys	
285 290 295	
cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca	1206
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro	
300 305 310	
ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa	1254
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu	
315 320 325	
gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc	1302

Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala  
 330 335 340 345  
 aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc 1350  
 Thr Glu Asp Gly Asp Ala Ser Pro Val Leu Asn His Ala Val 360  
 350  
 cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc 1398  
 Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly 375  
 365  
 atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg 1446  
 Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val 390  
 380 385  
 gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg 1494  
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg 405  
 395 400  
 agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca 1542  
 Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala 420  
 410 415 425  
 gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac 1590  
 Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp 430  
 435 440  
 tgg atc cac gag cag atg gag aga gac cta aaa acc tga agaggaaggg 1639  
 Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr \* 450  
 445  
 gataagtagc cacctga 1656  
 <210> 12  
 <211> 453  
 <212> PRT  
 <213> Homo Sapien  
 <400> 12  
 Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg  
 1 5 10 15  
 Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp  
 20 25 30  
 Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe  
 35 40 45  
 Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala  
 50 55 60  
 Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg  
 65 70 75 80  
 Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser  
 85 90 95  
 Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly  
 100 105 110  
 Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met  
 115 120 125  
 Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln  
 130 135 140  
 Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser  
 145 150 155 160  
 Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu  
 165 170 175  
 Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu

180 185 190  
 Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly  
 195 200 205  
 His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu  
 210 215 220  
 Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His  
 225 230 235 240  
 Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala  
 245 250 255  
 His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val  
 260 265 270  
 Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu  
 275 280 285  
 Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp  
 290 295 300  
 Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile  
 305 310 315 320  
 Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys  
 325 330 335  
 Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala  
 340 345 350  
 Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile  
 355 360 365  
 Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu  
 370 375 380  
 Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser  
 385 390 395 400  
 Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly  
 405 410 415  
 Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val  
 420 425 430  
 Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu  
 435 440 445  
 Arg Asp Leu Lys Thr  
 450

<210> 13  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide Primer

<221> misc\_feature  
 <222> (0)...(0)  
 <223> N= Inosine

<400> 13  
 tggtrtnvtnw sngcnrcnca ytg

23

<210> 14  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide Primer

<221> misc\_feature  
 <222> (0)...(0)  
 <223> N= Inosine

<400> 14  
 nggncncncn swrtcnccyt nrcanghrtc 30  
  
 <210> 15  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 15  
 tcaccgagaa gatgatgtgt gcaggcatcc 30  
  
 <210> 16  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 16  
 gggacagggg ctgtaaggca gggaaatgag 29  
  
 <210> 17  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 17  
 cccgcagcca tagccccagc taacg 25  
  
 <210> 18  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 18  
 gcagacgatg cgtaccaggg ggaagtc 27  
  
 <210> 19  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 19  
 ctcgagaaaa gagtgggtggg tggggaggag gcctctgtg 39  
  
 <210> 20  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer

<400> 20  
 gcggccgcat tacagctcag ccttcagac 30  
  
 <210> 21  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 21  
 cctccacggt gctgtggacc gtgttcc 27  
  
 <210> 22  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 22  
 cctcgcgcaa ggcgccccag cccg 24  
  
 <210> 23  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 23  
 gcgtggcgtc acctggtagc gatagacctc gc 32  
  
 <210> 24  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 24  
 cctccacggt gctgtggacc gtgttcc 27  
  
 <210> 25  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 25  
 cctcgcgcaa ggcgccccag cccg 24  
  
 <210> 26  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide Primer  
  
 <400> 26  
 tcacgcgcca gaggtgatc agtgag 26  
  
 <210> 27  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 27  
 cctcctcagt gcataggcat caaaccag 28  
  
 <210> 28  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 28  
 tctctcgaga aaagaattgt tgggtggagct gtgtcctccg ag 42  
  
 <210> 29  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 29  
 aggtgggcct tgctttgcag gggggcagtt c 31  
  
 <210> 30  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 30  
 tcacgcacgc tgggtggaac atgtcc 26  
  
 <210> 31  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 31  
 acccacctcc atctgctcgt ggatcc 26  
  
 <210> 32

<211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 32  
 ccacagcctc ctctcttgac acaccag 27  
  
 <210> 33  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 33  
 acgccccctgt ggatcatcac tgctgc 26  
  
 <210> 34  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 34  
 tccctccctc acatatactg agtggtg 27  
  
 <210> 35  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 35  
 cgactgctca ggaagtcag atgtcg 26  
  
 <210> 36  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 36  
 gcggccgcac tataccccag tgttctcttt gatcca 36  
  
 <210> 37  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer

<400> 37  
 ctggtgtgtc aagagaggag gctgtgg 27  
  
 <210> 38  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer  
  
 <400> 38  
 actcaggtgg ctacttatcc ccttcctc 28  
  
 <210> 39  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 39  
 tctctcgaga aaagagtggg ggggtggggag gaggcctctg tg 42  
  
 <210> 40  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 40  
 attcgcggcc gcattacagc tcagccttcc agac 34  
  
 <210> 41  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 41  
 tctctcgaga aaagaattgt tgggtggagct gtgtcctccg ag 42  
  
 <210> 42  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 42  
 attcgcggcc gctcaggtca ccacttgctg gatccag 37  
  
 <210> 43  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide Primer

&lt;400&gt; 43

ctcgagaaac gcacgtggg tggaacatg tccttg

36

&lt;210&gt; 44

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide Primer

&lt;400&gt; 44

actcaggtgg ctacttatcc ccttcctc

28

&lt;210&gt; 45

&lt;211&gt; 9276

&lt;212&gt; DNA

&lt;213&gt; Pichia pastoris

&lt;400&gt; 45

agatctaaca	tccaaagacg	aaagggttgaa	tgaaaccttt	ttgccatccg	acatccacag	60
gtccattctc	acacataagt	gccaaacgca	acaggagggg	atacactagc	agcagaccgt	120
tgcaaacgca	ggacctccac	tctctctctc	ctcaacaccc	acttttgcca	tcgaaaaacc	180
agcccagtta	ttgggcttga	ttggagctcg	ctcattccaa	ttccttctat	taggctacta	240
acaccatgac	tttattagcc	tgtctatcct	ggccccctcg	gcgaggttca	tgtttgttta	300
tttccgaatg	caacaagctc	cgcattacac	ccgaacatca	ctccagatga	gggctttctg	360
agtgtggggg	caaatagttt	catgttcccc	aaatggccca	aaactgacag	tttaaacgct	420
gtcttggaac	ctaatatgac	aaaagcgtga	tctcatccaa	gatgaactaa	gtttggttcg	480
ttgaaatgct	aacggccagt	tggtcaaaaa	gaaacttcca	aaagtcgcca	taccgtttgt	540
cttgtttggt	attgattgac	gaatgctcaa	aaataatctc	attaatgctt	agcgagctct	600
ctctatcgct	tctgaacccc	gggtgcacctg	tgccgaaacg	caaatgggga	aacacccgct	660
ttttggatga	ttatgcattg	tctccacatt	gtatgcttcc	aagattctgg	tggaataact	720
gctgatagcc	taacgttcat	gatcaaaaatt	taactgttct	aacccctact	tgacagcaat	780
atataaacag	aaggaagctg	ccctgtctta	aacctttttt	tttatcatca	ttattagctt	840
actttcataa	ttgcgactgg	ttccaattga	caagcttttg	atthtaacga	ctthtaacga	900
caacttgaga	agatcaaaaa	acaactaatt	attcgaagga	tccaaacgat	gagatttcct	960
tcaattttta	ctgcagtttt	attcgcagca	tcttcgcgat	tagctgctcc	agtcaacact	1020
acaacagaag	atgaaacggc	acaaaattccg	gctgaagctg	tcacgggtta	ctcagattta	1080
gaaggggatt	tcgatgttgc	tgttttgcca	ttttccaaca	gcacaaataa	cgggttattg	1140
tttataaata	ctactattgc	cagcatttgc	gctaaagaag	aaggggtatc	tctcgagaaa	1200
agagaggctg	aagcttacgt	agaattccct	agggcgggccg	cgaattaatt	cgccttagac	1260
atgactgttc	ctcagttcaa	gttgggcact	tacgagaaga	ccggtcttgc	tagattctaa	1320
tcaagaggat	gtcagaatgc	catttgccctg	agagatgcag	gcttcatttt	tgatactttt	1380
ttatttgtaa	cctatatagt	ataggatttt	ttttgtcatt	ttgtttcttc	tcgtacgagc	1440
ttgctcctga	tcagcctatc	tcgcagctga	tgaatatctt	gtggtagggg	tttgggaaaa	1500
tcattcgagt	ttgatgtttt	tcttggtatt	tcccactcct	cttcagagta	cagaagatta	1560
agtgagaagt	tcgtttgtgc	aagcttatcg	ataagcttta	atgcggtagt	ttatcacagt	1620
taaaattgcta	acgcagtcag	gcaccgtgta	tgaaatctaa	caatgcgctc	atcgatcatc	1680
tcggcaccgt	caccctggat	gctgtaggca	taggcttggt	tatgccggta	ctgccgggcc	1740
tcttgccgga	tatcgtccat	tccgacagca	tcgccagtca	ctatggcggtg	ctgctagcgc	1800
tatatgcgtt	gatgcaattt	ctatgcgcac	ccgttctcgg	agcactgtcc	gaccgctttg	1860
gccgccgccc	agtcctgtct	gcttcgctac	ttggagccac	tatcgactac	gcgatcatgg	1920
cgaccacacc	cgtcctgtgg	atctatcgaa	tctaaaatga	agttaaaatc	tctaaataat	1980
taaataagtc	ccagtttctc	catacgaacc	ttaacagcat	tgcggtgagc	atctagacct	2040
tcaacagcag	ccagatccat	cactgcttgg	ccaatatgtt	tcagtccctc	aggagttagc	2100
tcttggtgaag	tgatgaactt	ctggaagggt	gcagtgttaa	ctccgctgta	ttgacgggca	2160
tatccgtacg	ttggcaaagt	gtggttggtg	ccggaggagt	aatctccaca	actctctgga	2220
gagtaggcac	caacaaacac	agatccagcg	tgttgtactt	gatcaacata	agaagaagca	2280
ttctcgattt	gcaggatcaa	gtgttcagga	gcgtactgat	tggaacattt	caaagcctgc	2340

tcgtaggttg	caaccgatag	ggttgtagag	tggtcaatac	acttgcgtag	aatttcaacc	2400
cttggaact	gcacagcttg	ggttggaaca	gcatcttcaa	ttctggcaag	ctccttgtct	2460
gtcatatcga	cagccaacag	aatcacctgg	gaatcaatac	catggttcagc	ttgagacaga	2520
aggtctgagg	caacgaaatc	tggatcagcg	tatttatcag	caataactag	aacttcagaa	2580
ggcccagcag	gcatgtcaat	actacacagg	gctgatgtgt	cattttgaac	catcatcttg	2640
gcagcagtaa	cgaactgggt	tcctggacca	aataatttgt	cacacttagg	aacagtttct	2700
gttcgtaag	ccatagcagc	tactgcctgg	gcgcctcctg	ctagcacgat	acacttagca	2760
ccaaccttgt	gggcaacgta	gatgacttct	ggggtaaggg	taccatcctt	cttaggtgga	2820
gatgcaaaaa	caatttcttt	gcaaccagca	actttggcag	gaacaccag	catcagggaa	2880
gtggaaggca	gaattgcggt	tcaccaggga	atatagaggc	caactttctc	aataggctt	2940
gcaaacgag	agcagactac	accaggggcaa	gtctcaactt	gcaacgtctc	cgttagttag	3000
gcttcatgga	atttcttgac	gttatctata	gagagatcaa	tggctctctt	aacgttatct	3060
ggcaattgca	taagttcctc	tgggaaagga	gcttctaaca	cagggtgtctt	caaagcgact	3120
ccatcaaaat	tggcagttag	ttctaaaagg	gctttgtcac	cattttgacg	aacattgtcg	3180
acaattgggt	tgactaattc	cataatctgt	tcctgtttct	ggataggacg	acgaagggca	3240
tcttcaattt	cttgtgagga	ggccttagaa	acgtcaattt	tgcacaattc	aatacgacct	3300
tcagaaggga	cttcttttag	tttgatttct	tcttttaggtt	gttccttggt	gtatcctggc	3360
ttggcatctc	ctttccttct	agtgccttct	agggacttca	tatccaggtt	tctctccacc	3420
tcgtccacag	tcacaccgta	cttggcacat	ctaactaatg	caaaaataaaa	taagtacgca	3480
catctccagg	ctatatcttc	cttggattta	gcttctgcaa	gttcatcagc	ttctctcccta	3540
attttagcgt	tcaacaaaac	ttcgtcgtca	aataaccggt	tgggtataaga	accttctgga	3600
gcattgtctt	tacgatccca	caaggtggct	tccatggctc	taagaccctt	tgattggcca	3660
aaacaggaag	tgcgttccaa	gtgacagaaa	ccaacacctg	tttgttcaac	cacaaatttc	3720
aagcagtcct	catcacaatc	caagcaactc	cccagcaact	tttgagttgc	tccagatgta	3780
gcacctttat	accacaaaac	gtgacgacga	gattggtaga	ctccagtttg	tgtccttata	3840
gcctccggaa	tagacttttt	ggacgagtag	accaggccca	acgagtaatt	agaagagtca	3900
gccaccaaa	tagtgaatag	accatcgggg	cggtcagtag	tcaaagacgc	caacaaaatt	3960
tcaactgacg	ggaacttttt	gacatcttca	gaaagttcgt	attcagtagt	caattgccga	4020
gcatacaata	tggggattat	accagaagca	acagtggaa	tcacatctac	caactttgcg	4080
gtctcagaaa	aagcataaac	agttctacta	ccgccattag	tgaacttttt	caaactcgcc	4140
agtggagaag	aaaaaggcac	agcgatacta	gcattagcgg	gcaaggatgc	aacttttatca	4200
accaggggtc	tatagataac	cctagcgcct	gggatcatcc	tttggaaca	tctttctgcc	4260
aaatctaggt	ccaaaatcac	ttcattgata	ccattattgt	acaacttgag	caagttgtcg	4320
atcagctcct	caaattgggt	ctctgtaacg	gatgactcaa	cttgacacatt	aacttgaagc	4380
tcagtcgatt	gagtgaactt	gatcaggttg	tgcagctggt	cagcagcata	gggaaacacg	4440
gcttttctta	ccaaactcaa	ggaattatca	aactctgcaa	cacttgcgta	tgcaggtagc	4500
aagggaaatg	tcatacttga	agtcggacag	tgagtgtagt	cttgagaaat	tctgaagccg	4560
tatttttatt	atcagtgagt	cagtcacatc	gagatcctct	acgcgggacg	catcgtggcc	4620
gacctgcagg	gggggggggg	gcgctgaggt	ctgcctcgtg	aagaagggtgt	tgtgactca	4680
taccaggcct	gaatcgcccc	atcatccagc	cagaaagtga	gggagccacg	gttgatgaga	4740
gctttgttgt	aggtggacca	ggttggtgatt	ttgaactttt	gctttgccac	ggaacggctt	4800
gcgttgtcgg	gaagatgcgt	gatctgatcc	ttcaactcag	caaaaagttcg	atattattca	4860
caaagccggc	gtcccgtcaa	gtcagcgtaa	tgtcttgcca	gtgttacaac	caattaacca	4920
attctgatta	gaaaaactca	tcgagcatca	aatgaaactg	caatttatct	atatcaggat	4980
tatcaatacc	atatttttga	aaaagccggt	tctgtaatga	aggagaaaa	tcaccgaggg	5040
agttccatag	gatggcaaga	tcctggtatc	ggtctgcgat	tccgactcgt	ccaacatcaa	5100
tacaacctat	taattttccc	tcgtcaaaaa	taaggttatc	aagtgagaaa	tcaccatgag	5160
tgacgactga	atccggtgag	aatggcaaaa	gcttatgcat	ttctttccag	acttggtcaa	5220
caggccagcc	attacgctcg	tcatcaaaat	cactcgcac	aaccaaaaccg	ttattcattc	5280
gtgattgcgc	ctgagcgaga	cgaaatacgc	gatcgctggt	aaaaggacaa	ttacaaacag	5340
gaatcgaatg	caaccggcgc	aggaacactg	ccagcgcac	aacaatattt	tcacctgaat	5400
caggatattc	ttctaatacc	tggaaatgctg	ttttccgggg	gatcgcagtg	gtgagtaacc	5460
atgcatcatc	aggagtacgg	ataaaaatgct	tgatggctcg	aagaggcata	aattccgtca	5520
gccagtttag	tctgaccatc	tcatctgtaa	catcattggc	aacgctacct	ttgccatggt	5580
tcagaaacaa	ctctggcgca	tcgggcttcc	catacaatcg	atagattgtc	gcacctgatt	5640
gcccgcacatt	atcgcgagcc	catttatacc	catataaatc	agcatccatg	ttggaattta	5700
atcgcggcct	cgagcaagac	gtttccggtt	gaatatggct	cataacaccc	cttgtattac	5760
tgtttatgta	agcagacagt	tttattgttc	atgatgatat	atttttatct	tgtgcaatgt	5820
aacatcagag	attttgagac	acaacgtggc	tttccccccc	ccccctgcag	gtcggcatca	5880
ccggcgccac	aggtgcgggt	gctggcgctt	atatcgccga	catcacccgat	ggggaagatc	5940
gggctcgcca	cttcgggctc	atgagcgctt	gtttcgcggt	gggtatggtg	gcaggccccg	6000
tggccggggg	actgttgggc	gccatctcct	tgcagtcacc	attccttgcg	gcggcggtgc	6060

tcaacggcct	caacctacta	ctgggctgct	tcctaagtca	ggagtcgcat	aagggagagc	6120
gtcagagtac	tatgattgga	agtatgggaa	tggtgatacc	cgcattcttc	agtgtcttga	6180
gggtctcctat	cagattatgc	ccaactaaag	caaccggagg	aggagatttc	atggtaaatt	6240
tctctgactt	ttggatcatca	gtagactcga	actgtgagac	tatctcgggt	atgacagcag	6300
aaatgtcctt	cttggagaca	gtaaatgaag	tcccaccaat	aaagaaatcc	ttgttatcag	6360
gaacaaactt	cttgttttcga	acttttttcgg	tgctttgaac	tataaaatgt	agagtggata	6420
tgtcgggtag	gaatggagcg	ggcaaatgct	taccttctgg	accttcaaga	ggtagtagg	6480
gtttgtagat	actgatgcc	acttcagtga	caacgttgct	atttcgttca	aaccattccg	6540
aatccagaga	aatcaaagtt	gtttgtctac	tattgatcca	agccagtgcg	gtcttgaaac	6600
tgacaatagt	gtgctcgtgt	tttgagggtca	tctttgtatg	aataaatcta	gtctttgatc	6660
taaataatct	tgacgagcca	aggcgataaa	tacccaaatc	taaaactctt	ttaaaacggt	6720
aaaaggacaa	gtatgtctgc	ctgtattaaa	ccccaaatca	gctcgtagtc	tgatcctcat	6780
caacttgagg	ggcactatct	tgtttttagag	aaatttgccg	agatgcgata	tcgagaaaaa	6840
ggtagcgtga	ttttaaacgt	gaaattttatc	tcaagatctc	tgccctcgcg	gtttcggtag	6900
tgacggtgaa	aacctctgac	acatgcagct	cccggagacg	gtcacagctt	gtctgtaagc	6960
ggatgcccgg	agcagacaag	cccgtcaggg	cgcgtcagcg	gggtgtggcg	gggtgcgggg	7020
cgcagccatg	accagtcac	gtagcgatag	cggagtgtat	actggcttaa	ctatgcggca	7080
tcagagcaga	ttgtactgag	agtgcacct	atgctgggtg	aaataccgca	cagatgcgta	7140
aggagaaaat	accgcatcag	gcgctcttcc	gcttcctcgc	tcactgactc	gctgcgctcg	7200
gtcgttcggc	tgcggcgagc	gggtatcagct	cactcaaagg	cggtaataacg	gttatccaca	7260
gaatcagggg	ataacgcagg	aaagaacatg	tgagcaaaag	gccagcaaaa	ggccaggaac	7320
cgtaaaaagg	ccgcgttgct	ggcggttttcc	cataggctcc	gccccctga	cgagcatcac	7380
aaaaatcgac	gctcaagtca	gaggtggcga	aaccgcagag	gactataaag	ataccaggcg	7440
tttccccctg	gaagctccct	cgtgcgctct	cctgttccga	ccctgcccgt	taccggatac	7500
ctgtcccgct	ttctcccttc	gggaagcgtg	gcgctttctc	aatgctcacg	ctgtaggtat	7560
ctcagttcgg	tgtaggtcgt	tcgctccaag	ctgggctgtg	tgacgaacc	ccccgttcag	7620
cccagccgct	gcgccttatc	cggtaactat	cgtcttgagt	ccaacccggg	aagacacgac	7680
ttatcgccac	tggcagcagc	cactggtaac	aggattagca	gagcgaggta	tgtaggcggg	7740
gctacagagt	tcttgaagtg	gtggcctaac	tacggctaca	ctagaaggac	agtatttggg	7800
atctgcgctc	tgttgaagcc	agttaccttc	ggaaaaagag	ttggtagctc	ttgatccggc	7860
aaacaaacca	ccgctggtag	cgggtgggttt	tttggtttgca	agcagcagat	tacgcgcaga	7920
aaaaaaggat	ctcaagaaga	tcctttgatc	ttttctacgg	gggtctgacgc	tcagtggaaac	7980
gaaaactcac	gttaagggat	tttggctatg	agattatcaa	aaaggatctt	cacctagatc	8040
cttttaaaatt	aaaaatgaag	tttttaaatca	atctaaagta	tatatgagta	aacttgggtc	8100
gacagttacc	aatgcttaat	cagtgaaggca	cctatctcag	cgatctgtct	atttcgttca	8160
tccatagttg	cctgactccc	cgtcgtgtag	ataactacga	tacgggaggg	cttaccatct	8220
ggccccagtg	ctgcaatgat	accgcgagac	ccacgctcac	cggctccaga	tttatcagca	8280
ataaaccagg	cagccggaag	ggccgagcgc	agaagtggtc	ctgcaacttt	atccgcctcc	8340
atccagtcct	ttaatgttg	ccgggaagct	agagtaagta	gttcgccagt	taatagtttg	8400
cgcaacggtg	ttgccattgc	tgcaggcatc	gtgggtgtcac	gctcgtcgtt	tggtatggct	8460
tcattcagct	ccgggttccc	acgatcaagg	cgagttacat	gatcccccat	gttgtgcaaa	8520
aaagcgggtg	gctccttcgg	tcctccgatc	gttgtcagaa	gtaagttggc	cgcagtgtta	8580
tcactcatgg	ttatggcagc	atgcataat	tccttacttg	tcatgccatc	cgtaagatgc	8640
ttttctgtga	ctgggtgagta	ctcaaccaag	tcattctgag	aatagtgtat	gcggcgaccg	8700
agttgctctt	gcccggcgct	aacacgggat	aataccgcgc	cacatagcag	aactttaaaa	8760
gtgctcatca	ttggaaaacg	ttcttcgggg	cgaaaactct	caaggatctt	accgctgttg	8820
agatccagtt	cgatgtaacc	cactcgtgca	cccaactgat	cttcagcatc	ttttactttc	8880
accagcgttt	ctgggtgagc	aaaaacagga	aggcaaaatg	ccgcaaaaaa	gggaataagg	8940
gcgacacgga	aatggtgaat	actcatactc	ttcctttttc	aatattattg	aagcattttat	9000
cagggttatt	gtctcatgag	cggatacata	tttgaatgta	tttagaaaaa	taaacaaata	9060
ggggttccgc	gcacattttc	cggaaaagtg	ccacctgacg	tctaagaaac	cattattatc	9120
atgacattaa	cctataaaaa	taggcgtatc	acgagggcct	ttcgtcttca	agaattaatt	9180
ctcatgtttg	acagcttatc	atcgataagc	tgactcatgt	tggtattgtg	aaatagacgc	9240
agatcgggaa	cactgaaaaa	taacagttat	tattcgc			9276

&lt;210&gt; 46

&lt;211&gt; 3908

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 46

agcgcccaat acgcaaaccg cctctccccg cgcgttggcc gattcattaa tgcagctggc

60

acgacaggtt	tcccgactgg	aaagcgggca	gtgagcgcaa	cgcaattaat	gtgagttagc	120
tcactcatta	ggcaccaccg	gctttacact	ttatgcttcc	ggctcgtatg	ttgtgtggaa	180
ttgtgagcgg	ataacaattt	cacacaggaa	acagctatga	ccatgattac	gccaagcttg	240
gtaccgagct	cggatccact	agtaacggcc	gccagtgtgc	tggaattcgc	ccttaagggc	300
gaattctgca	gatatccatc	acactggcgg	ccgctcgagc	atgcatctag	agggcccaat	360
tcgccctata	gtgagtcgta	ttacaattca	ctggccgtcg	ttttacaacg	tcgtgactgg	420
gaaaaccctg	gcgttaccca	acttaatcgc	cttgacgac	atcccccttt	cgccagctgg	480
cgtaatagcg	aagaggcccc	caccgatcgc	ccttcccaac	agttgcgcag	cctgaatggc	540
gaatgggacg	cgccctgtag	cggcgcatta	agcgcggcgg	gtgtggtggt	tacgcgcagc	600
gtgaccgcga	cacttgccag	cgccctagcg	cccgctcctt	tcgctttctt	cccttccttt	660
ctcgccacgt	tcgcgcgctt	tccccgtcaa	gctctaaatc	gggggctccc	tttaggggtt	720
cgatttagag	ctttacggca	cctcgaccgc	aaaaaacttg	atttgggtga	tgggtcaagt	780
agtggggccat	cgccctgata	gacggttttt	cgccctttga	cgttggagtc	caggttcttt	840
aatagtggac	tcttgttcca	aactggaaca	acactcaacc	ctatcgcggt	ctattctttt	900
gattttataag	ggattttgcc	gatttcggcc	tattgggttaa	aaaatgagct	gatttaacaa	960
attcagggcg	caaggggtgc	taaaggaaac	ggaacacgta	gaaagccagt	ccgcagaaac	1020
ggtgctgacc	ccggatgaat	gtcagctact	gggctatctg	gacaagggaa	aacgcaagcg	1080
caaagagaaa	gcaggtagct	tgcagtgggc	ttacatggcg	atagctagac	tgggcgggtt	1140
tatggacagc	aagcgaaccg	gaattgccag	ctggggcgcc	ctctggtaag	gttgggaagc	1200
cctgcaagct	aaactggatg	gctttcttgc	cgccaaggat	ctgatggcgc	aggggatcaa	1260
gatctgatca	agagacagga	tgaggatcgt	ttcgcatgat	tgaacaagat	ggattgcacg	1320
cagggttctcc	ggccgcttgg	gtggagaggc	tattcggcta	tgactgggca	caacagacaa	1380
tcggctgctc	tgatgccgcc	gtgttcgggc	tgtcagcgca	ggggcgcccg	gttctttttg	1440
tcaagaccga	cctgtccggg	gccctgaatg	aactgcagga	cgaggcagcg	cggctatcgt	1500
ggctggccac	gacgggcgtt	ccttgccgag	ctgtgctcga	cgttgtcact	gaagcgggaa	1560
gggactggct	gctattgggg	gaagtgccgg	ggcaggatct	cctgtcatct	cgccctgctc	1620
ctgccgagaa	agtatccatc	atggctgatg	caatgcggcg	gctgcatacg	cttgatccgg	1680
ctacctgccc	attcgaccac	caagcgaaac	atcgcatcga	gcgagcacgt	actcggatgg	1740
aagccgggtc	tgtcgatcag	gatgatctgg	acgaagagca	tcaggggctc	gcgccagccg	1800
aaactgttcg	caggctcaag	gcgcgcgatg	ccgacggcga	ggatctcgtc	gtgatccatg	1860
gcgatgcctg	cttgccgaat	atcatggtgg	aaaatggccg	cttttctgga	ttcaacgact	1920
gtggccgggt	gggtgtggcg	gaccgctatc	aggacatagc	gttggatacc	cgtgatattg	1980
ctgaagagct	tggcggcgaa	tgggctgacc	gcttcctcgt	gctttacggg	atcgccgctc	2040
ccgattcgca	gcgcatcgcc	ttctatcgcc	ttcttgacga	gttcttctga	attgaaaaag	2100
gaagagtatg	agtattcaac	atttccgtgt	cgcccttatt	cccttttttg	cggcattttg	2160
ccttcctgtt	tttgcctacc	cagaaacgct	ggtgaaagta	aaagatgctg	aagatcagtt	2220
gggtgcacga	gtgggttaca	tcgaactgga	tctcaacagc	ggtaagatcc	ttgagagttt	2280
tcgcccogaa	gaacgttttc	caatgatgag	cactttttaa	gttctgctat	gtcatacact	2340
attatcccg	attgacgcgg	ggcaagagca	actcggctgc	cgggcgcggt	attctcagaa	2400
tgacttggtt	gagtactcac	cagtcacaga	aaagcatctt	acggatggca	tgacagtaag	2460
agaattatgc	agtgtgccca	taaccatgag	tgataaacact	gcgggccaa	tacttctgac	2520
aacgatcgga	ggaccgaagg	agctaaccgc	ttttttgcac	aacatggggg	atcatgtaac	2580
tcgccttgat	cgttggggaa	cggagctgaa	tgaagccata	ccaaacgacg	agagtgcac	2640
cacgatgcct	gtagcaatgc	caacaacggt	gcgcaacta	ttactggcg	aactacttac	2700
tctagcttcc	cggaacaat	taatagactg	gatggaggcg	gataaagttg	caggaccact	2760
tctgcgctcg	gcccttccgg	ctggctgggt	tattgctgat	aaatctggag	ccggtgagcg	2820
tgggtctcgc	ggtatcattg	cagcactggg	gccagatggg	aagccctccc	gtatcgtagt	2880
tatctacacg	acggggagtc	aggcaactat	ggatgaacga	aatagacaga	tcgctgagat	2940
aggtgcctca	ctgattaagc	attggtaact	gtcagaccaa	gtttactcat	atatacttta	3000
gattgattta	aaacttcatt	tttaatttaa	aaggatctag	gtgaagatcc	tttttgataa	3060
tctcatgacc	aaaatccctt	aacgtgagtt	ttcgttccac	tgagcgtcag	accccgtaga	3120
aaagatcaaa	ggatcttctt	gagatccttt	tttctgcgc	gtaatctgct	gcttgcaaac	3180
aaaaaaaacca	ccgctaccag	cggtgggttt	tttgccggat	caagagctac	caactctttt	3240
tccgaaggta	actggcttca	gcagagcgca	gataccaaat	actgtccttc	tagtgtagcc	3300
gtagttaggc	caccacttca	agaactctgt	agcaccgcct	acatacctcg	ctctgcta	3360
cctgttacca	gtggctgctg	ccagtggcga	taagtctgtg	cttaccgggt	tggactcaag	3420
acgatagtta	ccggataaag	ccgagcggtg	gggtggaacg	gggggttcgt	gcacacagcc	3480
cagcttgagg	cgaacgacct	acaccgaact	gagataccta	cagcgtgagc	attgagaaag	3540
cgccacgctt	cccgaaggga	gaaaggcgga	caggatatccg	gtaagcggca	gggtcggaac	3600
aggagagcgc	acgaggggag	ttccaggggg	aaacgcctgg	tatctttata	gtcctgtcgg	3660
gtttcgccac	ctctgcaattg	agcgtcgatt	tttgctgatg	tcgtcagggg	ggcggagcct	3720
atggaaaaac	gccagcaacg	cggccttttt	acgggttcctg	gccttttgc	ggccttttgc	3780

tcacatgttc tttcctgcgt tateccctga ttctgtggat aaccgtatta ccgcctttga 3840  
 gtgagctgat accgctcgcc gcagccgaac gaccgagcgc agcgagtcag tgagcgagga 3900  
 agcggaag 3908

<210> 47  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer

<400> 47 46  
 ggaattccat atgccgcgct ttaaagtggg ggggtggggag gaggcc

<210> 48  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer

<400> 48 32  
 cgcgataccc gttacagctc agccttccag ac

<210> 49  
 <211> 3147  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> CDS  
 <222> (1865)...(2590)  
 <223> Nucleic acid sequence of protease domain of MTSP1

<400> 49  
 tcaagagcgg cctcggggta ccatggggag cgatcggggc cgcaagggcg gagggggccc 60  
 gaaggacttc ggcgcgggac tcaagtacaa ctcccggcac gagaaagtga atggcttgga 120  
 ggaaggcgtg gagttcctgc cagtcaacaa cgtcaagaag gtggaaaagc atggcccggg 180  
 gcgctgggtg gtgctggcag ccgtgctgat cggcctcctc ttggtcttgc tggggatcgg 240  
 cttcctggtg tggcatttgc agtaccggga cgtgcgtgtc cagaaggctc tcaatggcta 300  
 catgaggatc acaaattgaga attttgtgga tgcctacgag aactccaact cactgagtt 360  
 tgtaagcctg gccagcaagg tgaaggacgc gctgaagctg ctgtacagcg gagtccatt 420  
 cctgggcccc taccacaagg agtcggctgt gacggccttc agcgagggca gcgtcatcgc 480  
 ctactactgg tctgagttca gcatcccgca gcacctggtg gaggaggccg agcgcgtcat 540  
 ggccgaggag cgcgtagtca tgctgcccc gcgggcgcgc tccctgaagt cctttgtggt 600  
 cacctcagtg gtggctttcc ccacggactc caaaacagta cagaggaccc aggacaacag 660  
 ctgcagcttt ggcctgcacg cccgcggtgt ggagctgatg cgcttcacca cgcccggctt 720  
 ccctgacagc ccctaccccg ctcatgcccg ctgccagtgg gccctgcggg gggacgccga 780  
 ctcagtgtcg agcctcacct tccgcagctt tgaccttgcg tccctgcgacg agcgcggcag 840  
 cgacctggtg acggtgtaca acaccctgag ccccatggag cccacgccc tgggtgcagtt 900  
 gtgtggcacc taccctccct cctacaacct gaccttccac tccctccaga acgtcctgct 960  
 catcacactg ataaccaaca ctgagcggcg gcatcccggc tttgaggcca ccttcttcca 1020  
 gctgcctagg atgagcagct gtggaggccg cttacgtaaa gccaggggga cattcaacag 1080  
 cccctactac ccaggccact acccaccac cattgactgc acatggaaca ttgaggtgcc 1140  
 caacaaccag catgtgaagg tgagcttcaa attcttctac ctgctggagc ccggcgtgcc 1200  
 tgccggcacc tgccccaagg actacgtgga gatcaatggg gagaaatact gcggagagag 1260  
 gtcccagttc gtcgtcacca gcaacagcaa caagatcaca gttcgcttcc actcagatca 1320  
 gtccacacc gacaccggct tcttagctga atacctctcc tacgactcca gtgacccatg 1380  
 cccggggcag ttcacgtgcc gcacggggcg gtgtatccgg aaggagctgc gctgtgatgg 1440  
 ctgggcccag tgcaccgacc acagcgatga gctcaactgc agttgcgacg ccggccacca 1500

gttcacgtgc aagaacaagt tctgcaagcc cctcttcttggtgtgacgaca gtgtgaacga	1560
ctgctggagac aacagcgcgc agcaggggtg cagttgtccg gcccagacct tcaggtgttc	1620
caatgggaag tgcctctcga aaagccagca gtgcaatggg aaggacgact gtggggacgg	1680
gtccgacgag gcctcctgcc ccaaggtgaa cgtcgtcact tgtacaaac acacctaccg	1740
ctgcctcaat gggctctgct tgagcaaggg caaccctgag tgtgacggga aggaggactg	1800
tagcgacggc tcagatgaga aggactgcga ctgtgggctg cggtcattca cgagacaggc	1860
tcgt gtt gtt ggg ggc acg gat gcg gat gag ggc gag tgg ccc tgg cag	1909
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln	
1 5 10 15	
gta agc ctg cat gct ctg ggc cag ggc cac atc tgc ggt gct tcc ctc	1957
Val Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu	
20 25 30	
atc tct ccc aac tgg ctg gtc tct gcc gca cac tgc tac atc gat gac	2005
Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp	
35 40 45	
aga gga ttc agg tac tca gac ccc acg cag tgg acg gcc ttc ctg ggc	2053
Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly	
50 55 60	
ttg cac gac cag agc cag cgc agc gcc cct ggg gtg cag gag cgc agg	2101
Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg	
65 70 75	
ctc aag cgc atc atc tcc cac ccc ttc ttc aat gac ttc acc ttc gac	2149
Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp	
80 85 90 95	
tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc	2197
Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser	
100 105 110	
atg gtg cgg ccc atc tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc	2245
Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala	
115 120 125	
ggc aag gcc atc tgg gtc acg ggc tgg gga cac acc cag tat gga ggc	2293
Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly	
130 135 140	
act ggc gcg ctg atc ctg caa aag ggt gag atc cgc gtc atc aac cag	2341
Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln	
145 150 155	
acc acc tgc gag aac ctc ctg ccg cag cag atc acg ccg cgc atg atg	2389
Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met	
160 165 170 175	
tgc gtg ggc ttc ctc agc ggc ggc gtg gac tcc tgc cag ggt gat tcc	2437
Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser	
180 185 190	
ggg gga ccc ctg tcc agc gtg gag gcg gat ggg cgg atc ttc cag gcc	2485
Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala	
195 200 205	
ggt gtg gtg agc tgg gga gac ggc tgc gct cag agg aac aag cca ggc	2533
Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly	
210 215 220	

gtg tac aca agg ctc cct ctg ttt cgg gac tgg atc aaa gag aac act 2581  
 Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr  
 225 230 235

ggg gta tag gggccggggc caccctaatg tgtacacctg cggggccacc 2630  
 Gly Val \*  
 240

catcgtccac cccagtgtgc acgcctgcag gctggagact ggaccgctga ctgcaccagc 2690  
 gccccagaa catacactgt gaactcaatc tccagggtc caaatctgcc tagaaaacct 2750  
 ctgcgttcct cagcctccaa agtggagctg ggaggtagaa ggggaggaca ctggtggttc 2810  
 tactgaccca actgggggca aaggtttgaa gacacagcct ccccgccag cccaagctg 2870  
 ggccgaggcg cgtttgtgta tatctgcctc ccctgtctgt aaggagcagc gggaacggag 2930  
 cttcggagcc tcctcagtga aggtggtggg gctgccgat ctgggctgtg gggcccttgg 2990  
 gccacgctct tgaggaagcc caggctcgga ggaccctgga aaacagacgg gtctgagact 3050  
 gaaattgttt taccagctcc cagggtggac ttcagtgtgt gtatttgtgt aaatgggtaa 3110  
 aacaatttat ttctttttaa aaaaaaaaaa aaaaaaa 3147

<210> 50  
 <211> 241  
 <212> PRT  
 <213> Homo Sapien

<400> 50  
 Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val  
 1 5 10 15  
 Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile  
 20 25 30  
 Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg  
 35 40 45  
 Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu  
 50 55 60  
 His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu  
 65 70 75 80  
 Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr  
 85 90 95  
 Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met  
 100 105 110  
 Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly  
 115 120 125  
 Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr  
 130 135 140  
 Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr  
 145 150 155 160  
 Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys  
 165 170 175  
 Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly  
 180 185 190  
 Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly  
 195 200 205  
 Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val  
 210 215 220  
 Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly  
 225 230 235 240  
 Val

<210> 51  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleoide Primer  
  
 <400> 51  
 tctctcgaga aaagagtggg gggtgggtgg ggaggaggcc tctgtg 46  
  
 <210> 52  
 <211> 43  
 <212> DNA  
 <213> Aritificial sequence  
  
 <400> 52  
 gctcctcatc aaagaagggc agagagatgg gcctgactgt gcc 43  
  
 <210> 53  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleoide Primer  
  
 <400> 53  
 attcgcggcc gcattacagc tcagccttcc agac 34  
  
 <210> 54  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleoide Primer  
  
 <400> 54  
 ggcacagtca ggcccatctc tctgcccttc tttgatgagg agc 43  
  
 <210> 55  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleoide Primer  
  
 <400> 55  
 cacccttct tcaatgactt caccttcg 28  
  
 <210> 56  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleoide Primer  
  
 <400> 56  
 tacctctcct acgactcc 18  
  
 <210> 57  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide Primer  
  
 <400> 57  
 gaggttctcg caggtggtct ggttg 25  
  
 <210> 58  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer  
  
 <400> 58  
 ctcgagaaaa gagttggttg gggcacggat gcggatgag 39  
  
 <210> 59  
 <211> 11  
 <212> PRT  
 <213> Homo Sapien  
  
 <400> 59  
 Phe Glu Val Phe Ser Gln Ser Ser Ser Leu Gly  
 1 5 10  
  
 <210> 60  
 <211> 32  
 <212> PRT  
 <213> Homo Sapien  
  
 <400> 60  
 Glu Ile Val Ala Pro Arg Glu Arg Ala Asp Arg Arg Gly Arg Lys Leu  
 1 5 10 15  
 Leu Cys Trp Arg Lys Pro Thr Lys Met Lys Gly Pro Arg Pro Ser His  
 20 25 30  
  
 <210> 61  
 <211> 4933  
 <212> DNA  
 <213> Homo Sapien  
  
 <220>  
 <221> CDS  
 <222> (94)...(3222)  
 <223> Nucleotide sequence encoding corin  
  
 <300>  
 <308> GenBank AF133845  
 <309> 1999-05-24  
  
 <400> 61  
 aaatcatccg tagtgctcc ccgggggaca cgtagaggag agaaaagcga ccaagataaa 60  
 agtggacaga agaataagcg agacttttta tcc atg aaa cag tct cct gcc ctc 114  
 Met Lys Gln Ser Pro Ala Leu  
 1 5  
  
 gct ccg gaa gag cgc tac cgc aga gcc ggg tcc cca aag ccg gtc ttg 162  
 Ala Pro Glu Glu Arg Tyr Arg Arg Ala Gly Ser Pro Lys Pro Val Leu  
 10 15 20  
  
 aga gct gat gac aat aac atg ggc aat ggc tgc tct cag aag ctg gcg 210

Arg	Ala	Asp	Asp	Asn	Asn	Met	Gly	Asn	Gly	Cys	Ser	Gln	Lys	Leu	Ala		
	25					30					35						
act	gct	aac	ctc	ctc	cgg	ttc	cta	ttg	ctg	gtc	ctg	att	cca	tgt	atc	258	
Thr	Ala	Asn	Leu	Leu	Arg	Phe	Leu	Leu	Leu	Val	Leu	Ile	Pro	Cys	Ile	55	
40					45					50							
tgt	gct	ctc	gtt	ctc	ttg	ctg	gtg	atc	ctg	ctt	tcc	tat	gtt	gga	aca	306	
Cys	Ala	Leu	Val	Leu	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Val	Gly	Thr	70	
				60					65								
tta	caa	aag	gtc	tat	ttt	aaa	tca	aat	ggg	agt	gaa	cct	ttg	gtc	act	354	
Leu	Gln	Lys	Val	Tyr	Phe	Lys	Ser	Asn	Gly	Ser	Glu	Pro	Leu	Val	Thr	85	
			75					80									
gat	ggt	gaa	atc	caa	ggg	tcc	gat	gtt	att	ctt	aca	aat	aca	att	tat	402	
Asp	Gly	Glu	Ile	Gln	Gly	Ser	Asp	Val	Ile	Leu	Thr	Asn	Thr	Ile	Tyr	100	
		90					95										
aac	cag	agc	act	gtg	gtg	tct	act	gca	cat	ccc	gac	caa	cac	gtt	cca	450	
Asn	Gln	Ser	Thr	Val	Val	Ser	Thr	Ala	His	Pro	Asp	Gln	His	Val	Pro	115	
	105					110											
gcc	tgg	act	acg	gat	gct	tct	ctc	cca	ggg	gac	caa	agt	cac	agg	aat	498	
Ala	Trp	Thr	Thr	Asp	Ala	Ser	Leu	Pro	Gly	Asp	Gln	Ser	His	Arg	Asn	135	
120					125					130							
aca	agt	gcc	tgt	atg	aac	atc	acc	cac	agc	cag	tgt	cag	atg	ctg	ccc	546	
Thr	Ser	Ala	Cys	Met	Asn	Ile	Thr	His	Ser	Gln	Cys	Gln	Met	Leu	Pro	150	
				140					145								
tac	cac	gcc	acg	ctg	aca	cct	ctc	ctc	tca	gtt	gtc	aga	aac	atg	gaa	594	
Tyr	His	Ala	Thr	Leu	Thr	Pro	Leu	Leu	Ser	Val	Val	Arg	Asn	Met	Glu	165	
			155					160									
atg	gaa	aag	ttc	ctc	aag	ttt	ttc	aca	tat	ctc	cat	cgc	ctc	agt	tgc	642	
Met	Glu	Lys	Phe	Leu	Lys	Phe	Phe	Thr	Tyr	Leu	His	Arg	Leu	Ser	Cys	180	
		170				175											
tat	caa	cat	atc	atg	ctg	ttt	ggc	tgt	acc	ctc	gcc	ttc	cct	gag	tgc	690	
Tyr	Gln	His	Ile	Met	Leu	Phe	Gly	Cys	Thr	Leu	Ala	Phe	Pro	Glu	Cys	195	
	185					190											
atc	att	gat	ggc	gat	gac	agt	cat	gga	ctc	ctg	ccc	tgt	agg	tcc	ttc	738	
Ile	Ile	Asp	Gly	Asp	Asp	Ser	His	Gly	Leu	Leu	Pro	Cys	Arg	Ser	Phe	215	
200					205					210							
tgt	gag	gct	gca	aaa	gaa	ggc	tgt	gaa	tca	gtc	ctg	ggg	atg	gtg	aat	786	
Cys	Glu	Ala	Ala	Lys	Glu	Gly	Cys	Glu	Ser	Val	Leu	Gly	Met	Val	Asn	230	
				220					225								
tac	tcc	tgg	ccg	gat	ttc	ctc	aga	tgc	tcc	cag	ttt	aga	aac	caa	act	834	
Tyr	Ser	Trp	Pro	Asp	Phe	Leu	Arg	Cys	Ser	Gln	Phe	Arg	Asn	Gln	Thr	245	
			235					240									
gaa	agc	agc	aat	gtc	agc	aga	att	tgc	ttc	tca	cct	cag	cag	gaa	aac	882	
Glu	Ser	Ser	Asn	Val	Ser	Arg	Ile	Cys	Phe	Ser	Pro	Gln	Gln	Glu	Asn	260	
		250					255										
gga	aag	caa	ttg	ctc	tgt	gga	agg	ggt	gag	aac	ttt	ctg	tgt	gcc	agt	930	
Gly	Lys	Gln	Leu	Leu	Cys	Gly	Arg	Gly	Glu	Asn	Phe	Leu	Cys	Ala	Ser	275	
	265					270											

gga atc tgc atc ccc ggg aaa ctg caa tgt aat ggc tac aac gac tgt	978
Gly Ile Cys Ile Pro Gly Lys Leu Gln Cys Asn Gly Tyr Asn Asp Cys	
280 285 290 295	
gac gac tgg agt gac gag gct cat tgc aac tgc agc gag aat ctg ttt	1026
Asp Asp Trp Ser Asp Glu Ala His Cys Asn Cys Ser Glu Asn Leu Phe	
300 305 310	
cac tgt cac aca ggc aag tgc ctt aat tac agc ctt gtg tgt gat gga	1074
His Cys His Thr Gly Lys Cys Leu Asn Tyr Ser Leu Val Cys Asp Gly	
315 320 325	
tat gat gac tgt ggg gat ttg agt gat gag caa aac tgt gat tgc aat	1122
Tyr Asp Asp Cys Gly Asp Leu Ser Asp Glu Gln Asn Cys Asp Cys Asn	
330 335 340	
ccc aca aca gag cat cgc tgc ggg gac ggg cgc tgc atc gcc atg gag	1170
Pro Thr Thr Glu His Arg Cys Gly Asp Gly Arg Cys Ile Ala Met Glu	
345 350 355	
tgg gtg tgt gat ggt gac cac gac tgt gtg gat aag tcc gac gag gtc	1218
Trp Val Cys Asp Gly Asp His Asp Cys Val Asp Lys Ser Asp Glu Val	
360 365 370 375	
aac tgc tcc tgt cac agc cag ggt ctg gtg gaa tgc aga aat gga caa	1266
Asn Cys Ser Cys His Ser Gln Gly Leu Val Glu Cys Arg Asn Gly Gln	
380 385 390	
tgt atc ccc agc acg ttt caa tgt gat ggt gac gag gac tgc aag gat	1314
Cys Ile Pro Ser Thr Phe Gln Cys Asp Gly Asp Glu Asp Cys Lys Asp	
395 400 405	
ggg agt gat gag gag aac tgc agc gtc att cag act tca tgt caa gaa	1362
Gly Ser Asp Glu Glu Asn Cys Ser Val Ile Gln Thr Ser Cys Gln Glu	
410 415 420	
gga gac caa aga tgc ctc tac aat ccc tgc ctt gat tca tgt ggt ggt	1410
Gly Asp Gln Arg Cys Leu Tyr Asn Pro Cys Leu Asp Ser Cys Gly Gly	
425 430 435	
agc tct ctc tgt gac ccg aac aac agt ctg aat aac tgt agt caa tgt	1458
Ser Ser Leu Cys Asp Pro Asn Asn Ser Leu Asn Asn Cys Ser Gln Cys	
440 445 450 455	
gaa cca att aca ttg gaa ctc tgc atg aat ttg ccc tac aac agt aca	1506
Glu Pro Ile Thr Leu Glu Leu Cys Met Asn Leu Pro Tyr Asn Ser Thr	
460 465 470	
agt tat cca aat tat ttt ggc cac agg act caa aag gaa gca tcc atc	1554
Ser Tyr Pro Asn Tyr Phe Gly His Arg Thr Gln Lys Glu Ala Ser Ile	
475 480 485	
agc tgg gag tct tct ctt ttc cct gca ctt gtt caa acc aac tgt tat	1602
Ser Trp Glu Ser Ser Leu Phe Pro Ala Leu Val Gln Thr Asn Cys Tyr	
490 495 500	
aaa tac ctc atg ttc ttt tct tgc acc att ttg gta cca aaa tgt gat	1650
Lys Tyr Leu Met Phe Phe Ser Cys Thr Ile Leu Val Pro Lys Cys Asp	
505 510 515	
gtg aat aca ggc gag cgt atc cct cct tgc agg gca ttg tgt gaa cac	1698

Val 520	Asn	Thr	Gly	Glu	Arg 525	Ile	Pro	Pro	Cys	Arg 530	Ala	Leu	Cys	Glu	His 535	
tct Ser	aaa Lys	gaa Glu	cgc Arg	tgt Cys 540	gag Glu	tct Ser	gtt Val	ctt Leu	ggg Gly 545	att Ile	gtg Val	ggc Gly	cta Leu	cag Gln 550	tgg Trp	1746
cct Pro	gaa Glu	gac Asp	aca Thr 555	gat Asp	tgc Cys	agt Ser	caa Gln	ttt Phe 560	cca Pro	gag Glu	gaa Glu	aat Asn	tca Ser 565	gac Asp	aat Asn	1794
caa Gln	acc Thr	tgc Cys 570	ctg Leu	atg Met	cct Pro	gat Asp	gaa Glu 575	tat Tyr	gtg Val	gaa Glu	gaa Glu	tgc Cys 580	tca Ser	cct Pro	agt Ser	1842
cat His 585	ttc Phe	aag Lys	tgc Cys	cgc Arg	tca Ser	gga Gly 590	cag Gln	tgt Cys	gtt Val	ctg Leu	gct Ala 595	tcc Ser	aga Arg	aga Arg	tgt Cys	1890
gat Asp 600	ggc Gly	cag Gln	gcc Ala	gac Asp	tgt Cys 605	gac Asp	gat Asp	gac Asp	agt Ser	gat Asp 610	gag Glu	gaa Glu	aac Asn	tgt Cys	ggg Gly 615	1938
tgt Cys	aaa Lys	gag Glu	aga Arg	gat Asp 620	ctt Leu	tgg Trp	gaa Glu	tgt Cys	cca Pro 625	tcc Ser	aat Asn	aaa Lys	caa Gln	tgt Cys 630	ttg Leu	1986
aag Lys	cac His	aca Thr	gtg Val 635	atc Ile	tgc Cys	gat Asp	ggg Gly	ttc Phe 640	cca Pro	gac Asp	tgc Cys	cct Pro	gat Asp 645	tac Tyr	atg Met	2034
gac Asp	gag Glu	aaa Lys 650	aac Asn	tgc Cys	tca Ser	ttt Phe	tgc Cys 655	caa Gln	gat Asp	gat Asp	gag Glu	ctg Leu 660	gaa Glu	tgt Cys	gca Ala	2082
aac Asn 665	cat His	gcg Ala	tgt Cys	gtg Val	tca Ser	cgt Arg 670	gac Asp	ctg Leu	tgg Trp	tgt Cys	gat Asp 675	ggg Gly	gaa Glu	gcc Ala	gac Asp	2130
tgc Cys 680	tca Ser	gac Asp	agt Ser	tca Ser	gat Asp 685	gaa Glu	tgg Trp	gac Asp	tgt Cys	gtg Val 690	acc Thr	ctc Leu	tct Ser	ata Ile	aat Asn 695	2178
gtg Val	aac Asn	tcc Ser	tct Ser	tcc Ser	ttt Phe 700	ctg Leu	atg Met	gtt Val	cac His 705	aga Arg	gct Ala	gcc Ala	aca Thr	gaa Glu 710	cac His	2226
cat His	gtg Val	tgt Cys	gca Ala 715	gat Asp	ggc Gly	tgg Trp	cag Gln	gag Glu 720	ata Ile	ttg Leu	agt Ser	cag Gln	ctg Leu 725	gcc Ala	tgc Cys	2274
aag Lys	cag Gln	atg Met	ggg Gly	tta Leu	gga Gly	gaa Glu	cca Pro	tct Ser	gtg Val	acc Thr	aaa Lys	ttg Leu 740	ata Ile	cag Gln	gaa Glu	2322
cag Gln 745	gag Glu	aaa Lys	gag Glu	ccg Pro	cgg Arg	tgg Trp	ctg Leu	aca Thr	tta Leu	cac His	tcc Ser 755	aac Asn	tgg Trp	gag Glu	agc Ser	2370
ctc Leu 760	aat Asn	ggg Gly	acc Thr	act Thr	tta Leu 765	cat His	gaa Glu	ctt Leu	cta Leu	gta Val 770	aat Asn	ggg Gly	cag Gln	tct Ser	tgt Cys 775	2418

gag agc aga agt aaa att tct ctt ctg tgt act aaa caa gac tgt ggg Glu Ser Arg Ser Lys Ile Ser Leu Leu Cys Thr Lys Gln Asp Cys Gly	2466
780 785 790	
cgc cgc cct gct gcc cga atg aac aaa agg atc ctt gga ggt cgg acg Arg Arg Pro Ala Ala Arg Met Asn Lys Arg Ile Leu Gly Gly Arg Thr	2514
795 800 805	
agt cgc cct gga agg tgg cca tgg cag tgt tct ctg cag agt gaa ccc Ser Arg Pro Gly Arg Trp Pro Trp Gln Cys Ser Leu Gln Ser Glu Pro	2562
810 815 820	
agt gga cat atc tgt ggc tgt gtc ctc att gcc aag aag tgg gtt ctg Ser Gly His Ile Cys Gly Cys Val Leu Ile Ala Lys Lys Trp Val Leu	2610
825 830 835	
aca gtt gcc cac tgc ttc gag ggg aga gag aat gct gca gtt tgg aaa Thr Val Ala His Cys Phe Glu Gly Arg Glu Asn Ala Ala Val Trp Lys	2658
840 845 850 855	
gtg gtg ctt ggc atc aac aat cta gac cat cca tca gtg ttc atg cag Val Val Leu Gly Ile Asn Asn Leu Asp His Pro Ser Val Phe Met Gln	2706
860 865 870	
aca cgc ttt gtg aag acc atc atc ctg cat ccc cgc tac agt cga gca Thr Arg Phe Val Lys Thr Ile Ile Leu His Pro Arg Tyr Ser Arg Ala	2754
875 880 885	
gtg gtg gac tat gac atc agc atc gtt gag ctg agt gaa gac atc agt Val Val Asp Tyr Asp Ile Ser Ile Val Glu Leu Ser Glu Asp Ile Ser	2802
890 895 900	
gag act ggc tac gtc cgg cct gtc tgc ttg ccc aac ccg gag cag tgg Glu Thr Gly Tyr Val Arg Pro Val Cys Leu Pro Asn Pro Glu Gln Trp	2850
905 910 915	
cta gag cct gac acg tac tgc tat atc aca ggc tgg ggc cac atg ggc Leu Glu Pro Asp Thr Tyr Cys Tyr Ile Thr Gly Trp Gly His Met Gly	2898
920 925 930 935	
aat aaa atg cca ttt aag ctg caa gag gga gag gtc cgc att att tct Asn Lys Met Pro Phe Lys Leu Gln Glu Gly Glu Val Arg Ile Ile Ser	2946
940 945 950	
ctg gaa cat tgt cag tcc tac ttt gac atg aag acc atc acc act cgg Leu Glu His Cys Gln Ser Tyr Phe Asp Met Lys Thr Ile Thr Thr Arg	2994
955 960 965	
atg ata tgt gct ggc tat gag tct ggc aca gtt gat tca tgc atg ggt Met Ile Cys Ala Gly Tyr Glu Ser Gly Thr Val Asp Ser Cys Met Gly	3042
970 975 980	
gac agc ggt ggg cct ctt gtt tgt gag aag cct gga gga cgg tgg aca Asp Ser Gly Gly Pro Leu Val Cys Glu Lys Pro Gly Gly Arg Trp Thr	3090
985 990 995	
tta ttt gga tta act tca tgg ggc tcc gtc tgc ttt tcc aaa gtc ctg Leu Phe Gly Leu Thr Ser Trp Gly Ser Val Cys Phe Ser Lys Val Leu	3138
1000 1005 1010 1015	
ggg cct ggc gtt tat agt aat gtg tca tat ttc gtc gaa tgg att aaa	3186

Gly Pro Gly Val Tyr Ser Asn Val Ser Tyr Phe Val Glu Trp Ile Lys  
 1020 1025 1030

aga cag att tac atc cag acc ttt ctc cta aac taa ttataaggat 3232  
 Arg Gln Ile Tyr Ile Gln Thr Phe Leu Leu Asn \*  
 1035 1040

gatcagagac ttttgccagc tacactaaaa gaaaatggcc ttcttgactg tgaagagctg 3292  
 cctgcagaga gctgtacaga agcacttttc atggacagaa atgctcaatc gtgcactgca 3352  
 aatttgcattg tttgttttgg actaattttt ttcaatttat tttttcacct tcatttttct 3412  
 cttattttcaa gttcaatgaa agactttaca aaagcaaaca aagcagactt tgtccttttg 3472  
 ccaggcctaa ccatgactgc agcacaaaat tatcgactct ggcgagattt aaaatcaggt 3532  
 gctacagtaa caggttatgg aatggtctct tttatcctat cacaaaaaaa gacatagata 3592  
 ttttaggctga ttaattatct ctaccagttt ttgttttctca agctcagtg c atagtggtaa 3652  
 atttcagtg taacattgga gacttgcttt tctttttctt tttttatacc ccacaattct 3712  
 tttttattac acttcgaatt ttagggtaca cgagcacaa c gtgcagggtta gttacatatg 3772  
 tatacatgtg ccatgttggt gtgctgaacc cagtaactcg tcatttgatt tattaanaagc 3832  
 caagataatt tacatgttta aagtatttac tattaccccc ttctaattgt tgcataattc 3892  
 tgagaactga taaaagacag caataaaaaga ccagtgtcat ccatttaggt agcaagacat 3952  
 attgaatgca aagttcttta gatatacaata ttaacacttg acattattgg accccccatt 4012  
 ctggatgtat atcaagatca taattttata gaagagtctc tatagaactg tcctcatagc 4072  
 tgggtttgtt caggatatat gagttggctg attgagactg caacaactac atctatat 4132  
 atgggcaata ttttgtttta cttatgtggc aaagaactgg atattaaact ttgcaaaaaga 4192  
 gaatttagat gagagatgca attttttaaa aagaaaatta atttgcattc ctcgtttaat 4252  
 taaatttatt tttcagtttt cttgcgttca tccataccaa caaagtcata aagagcatat 4312  
 ttttagagcac agtaagactt tgcattggagt aaaacatttt gtaattttcc tcaaaaagatg 4372  
 ttttaatatct gggttcttct cattggtaat taaaatttta gaaatgattt ttagctctag 4432  
 gccactttac gcaactcaat ttctgaagca attagtggta aaaagtattt ttccccacta 4492  
 aaaaacttta aaacacaaat cttcatatat acttaattta attagtcagg catccatttt 4552  
 gcctttttaa caactaggat tccctactaa cctccaccag caacctggac tgcctcagca 4612  
 ttccaaatag atactacctg caattttata catgtatttt tgtatcttt ctgtgtgtaa 4672  
 acatagttga aattcaaaaa gttgttagcaa tttctatact attcatctcc tgtccttcag 4732  
 tttgtataaa cctaaggaga gtgtgaaatc cagcaactga attgtgggtca cgattgtatg 4792  
 aaagttcaag aacatatgtc agttttgtta cagttgtagc tacatactca atgtatcaac 4852  
 ttttagcctg ctcaacttag gctcagtgaa atatatatat tatacttatt ttaataaatt 4912  
 cttaatacaa ataaaatgggt a 4933

<210> 62  
 <211> 1042  
 <212> PRT  
 <213> Homo Sapien

<400> 62  
 Met Lys Gln Ser Pro Ala Leu Ala Pro Glu Glu Arg Tyr Arg Arg Ala  
 1 5 10 15  
 Gly Ser Pro Lys Pro Val Leu Arg Ala Asp Asp Asn Asn Met Gly Asn  
 20 25 30  
 Gly Cys Ser Gln Lys Leu Ala Thr Ala Asn Leu Leu Arg Phe Leu Leu  
 35 40 45  
 Leu Val Leu Ile Pro Cys Ile Cys Ala Leu Val Leu Leu Val Ile  
 50 55 60  
 Leu Leu Ser Tyr Val Gly Thr Leu Gln Lys Val Tyr Phe Lys Ser Asn  
 65 70 75 80  
 Gly Ser Glu Pro Leu Val Thr Asp Gly Glu Ile Gln Gly Ser Asp Val  
 85 90 95  
 Ile Leu Thr Asn Thr Ile Tyr Asn Gln Ser Thr Val Val Ser Thr Ala  
 100 105 110  
 His Pro Asp Gln His Val Pro Ala Trp Thr Thr Asp Ala Ser Leu Pro  
 115 120 125  
 Gly Asp Gln Ser His Arg Asn Thr Ser Ala Cys Met Asn Ile Thr His  
 130 135 140  
 Ser Gln Cys Gln Met Leu Pro Tyr His Ala Thr Leu Thr Pro Leu Leu

145	Ser	Val	Val	Arg	Asn	Met	Glu	Met	Glu	Lys	Phe	Leu	Lys	Phe	Phe	Thr
					165					170						175
Tyr	Leu	His	Arg	Leu	Ser	Cys	Tyr	Gln	His	Ile	Met	Leu	Phe	Gly	Cys	
			180						185					190		
Thr	Leu	Ala	Phe	Pro	Glu	Cys	Ile	Ile	Asp	Gly	Asp	Asp	Ser	His	Gly	
		195					200					205				
Leu	Leu	Pro	Cys	Arg	Ser	Phe	Cys	Glu	Ala	Ala	Lys	Glu	Gly	Cys	Glu	
	210					215					220					
Ser	Val	Leu	Gly	Met	Val	Asn	Tyr	Ser	Trp	Pro	Asp	Phe	Leu	Arg	Cys	
225					230					235					240	
Ser	Gln	Phe	Arg	Asn	Gln	Thr	Glu	Ser	Ser	Asn	Val	Ser	Arg	Ile	Cys	
				245					250					255		
Phe	Ser	Pro	Gln	Glu	Asn	Gly	Lys	Gln	Leu	Leu	Cys	Gly	Arg	Gly		
			260				265					270				
Glu	Asn	Phe	Leu	Cys	Ala	Ser	Gly	Ile	Cys	Ile	Pro	Gly	Lys	Leu	Gln	
		275					280					285				
Cys	Asn	Gly	Tyr	Asn	Asp	Cys	Asp	Asp	Trp	Ser	Asp	Glu	Ala	His	Cys	
	290					295					300					
Asn	Cys	Ser	Glu	Asn	Leu	Phe	His	Cys	His	Thr	Gly	Lys	Cys	Leu	Asn	
305					310					315					320	
Tyr	Ser	Leu	Val	Cys	Asp	Gly	Tyr	Asp	Asp	Cys	Gly	Asp	Leu	Ser	Asp	
				325					330					335		
Glu	Gln	Asn	Cys	Asp	Cys	Asn	Pro	Thr	Thr	Glu	His	Arg	Cys	Gly	Asp	
		340						345					350			
Gly	Arg	Cys	Ile	Ala	Met	Glu	Trp	Val	Cys	Asp	Gly	Asp	His	Asp	Cys	
		355					360					365				
Val	Asp	Lys	Ser	Asp	Glu	Val	Asn	Cys	Ser	Cys	His	Ser	Gln	Gly	Leu	
	370					375					380					
Val	Glu	Cys	Arg	Asn	Gly	Gln	Cys	Ile	Pro	Ser	Thr	Phe	Gln	Cys	Asp	
385					390					395					400	
Gly	Asp	Glu	Asp	Cys	Lys	Asp	Gly	Ser	Asp	Glu	Glu	Asn	Cys	Ser	Val	
				405					410					415		
Ile	Gln	Thr	Ser	Cys	Gln	Glu	Gly	Asp	Gln	Arg	Cys	Leu	Tyr	Asn	Pro	
			420					425					430			
Cys	Leu	Asp	Ser	Cys	Gly	Gly	Ser	Ser	Leu	Cys	Asp	Pro	Asn	Asn	Ser	
		435					440					445				
Leu	Asn	Asn	Cys	Ser	Gln	Cys	Glu	Pro	Ile	Thr	Leu	Glu	Leu	Cys	Met	
	450					455					460					
Asn	Leu	Pro	Tyr	Asn	Ser	Thr	Ser	Tyr	Pro	Asn	Tyr	Phe	Gly	His	Arg	
465					470					475					480	
Thr	Gln	Lys	Glu	Ala	Ser	Ile	Ser	Trp	Glu	Ser	Ser	Leu	Phe	Pro	Ala	
				485					490					495		
Leu	Val	Gln	Thr	Asn	Cys	Tyr	Lys	Tyr	Leu	Met	Phe	Phe	Ser	Cys	Thr	
			500					505					510			
Ile	Leu	Val	Pro	Lys	Cys	Asp	Val	Asn	Thr	Gly	Glu	Arg	Ile	Pro	Pro	
		515					520					525				
Cys	Arg	Ala	Leu	Cys	Glu	His	Ser	Lys	Glu	Arg	Cys	Glu	Ser	Val	Leu	
	530					535					540					
Gly	Ile	Val	Gly	Leu	Gln	Trp	Pro	Glu	Asp	Thr	Asp	Cys	Ser	Gln	Phe	
545					550					555					560	
Pro	Glu	Glu	Asn	Ser	Asp	Asn	Gln	Thr	Cys	Leu	Met	Pro	Asp	Glu	Tyr	
				565					570					575		
Val	Glu	Glu	Cys	Ser	Pro	Ser	His	Phe	Lys	Cys	Arg	Ser	Gly	Gln	Cys	
			580					585					590			
Val	Leu	Ala	Ser	Arg	Arg	Cys	Asp	Gly	Gln	Ala	Asp	Cys	Asp	Asp	Asp	
		595					600					605				
Ser	Asp	Glu	Glu	Asn	Cys	Gly	Cys	Lys	Glu	Arg	Asp	Leu	Trp	Glu	Cys	
	610					615					620					
Pro	Ser	Asn	Lys	Gln	Cys	Leu	Lys	His	Thr	Val	Ile	Cys	Asp	Gly	Phe	
625					630					635					640	
Pro	Asp	Cys	Pro	Asp	Tyr	Met	Asp	Glu	Lys	Asn	Cys	Ser	Phe	Cys	Gln	

```

        645              650              655
Asp Asp Glu Leu Glu Cys Ala Asn His Ala Cys Val Ser Arg Asp Leu
        660              665              670
Trp Cys Asp Gly Glu Ala Asp Cys Ser Asp Ser Ser Asp Glu Trp Asp
        675              680              685
Cys Val Thr Leu Ser Ile Asn Val Asn Ser Ser Ser Phe Leu Met Val
        690              695              700
His Arg Ala Ala Thr Glu His His Val Cys Ala Asp Gly Trp Gln Glu
705              710              715
Ile Leu Ser Gln Leu Ala Cys Lys Gln Met Gly Leu Gly Glu Pro Ser
        725              730              735
Val Thr Lys Leu Ile Gln Glu Gln Glu Lys Glu Pro Arg Trp Leu Thr
740              745              750
Leu His Ser Asn Trp Glu Ser Leu Asn Gly Thr Thr Leu His Glu Leu
        755              760              765
Leu Val Asn Gly Gln Ser Cys Glu Ser Arg Ser Lys Ile Ser Leu Leu
770              775              780
Cys Thr Lys Gln Asp Cys Gly Arg Arg Pro Ala Ala Arg Met Asn Lys
785              790              795
Arg Ile Leu Gly Gly Arg Thr Ser Arg Pro Gly Arg Trp Pro Trp Gln
        805              810              815
Cys Ser Leu Gln Ser Glu Pro Ser Gly His Ile Cys Gly Cys Val Leu
        820              825              830
Ile Ala Lys Lys Trp Val Leu Thr Val Ala His Cys Phe Glu Gly Arg
835              840              845
Glu Asn Ala Ala Val Trp Lys Val Val Leu Gly Ile Asn Asn Leu Asp
850              855              860
His Pro Ser Val Phe Met Gln Thr Arg Phe Val Lys Thr Ile Ile Leu
865              870              875
His Pro Arg Tyr Ser Arg Ala Val Val Asp Tyr Asp Ile Ser Ile Val
        885              890              895
Glu Leu Ser Glu Asp Ile Ser Glu Thr Gly Tyr Val Arg Pro Val Cys
900              905              910
Leu Pro Asn Pro Glu Gln Trp Leu Glu Pro Asp Thr Tyr Cys Tyr Ile
915              920              925
Thr Gly Trp Gly His Met Gly Asn Lys Met Pro Phe Lys Leu Gln Glu
930              935              940
Gly Glu Val Arg Ile Ile Ser Leu Glu His Cys Gln Ser Tyr Phe Asp
945              950              955
Met Lys Thr Ile Thr Thr Arg Met Ile Cys Ala Gly Tyr Glu Ser Gly
        965              970              975
Thr Val Asp Ser Cys Met Gly Asp Ser Gly Gly Pro Leu Val Cys Glu
980              985              990
Lys Pro Gly Gly Arg Trp Thr Leu Phe Gly Leu Thr Ser Trp Gly Ser
995              1000              1005
Val Cys Phe Ser Lys Val Leu Gly Pro Gly Val Tyr Ser Asn Val Ser
1010              1015              1020
Tyr Phe Val Glu Trp Ile Lys Arg Gln Ile Tyr Ile Gln Thr Phe Leu
1025              1030              1035
Leu Asn

```

<210> 63

<211> 3696

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (41)...(3100)

<223> Nucleotide sequence encoding human entorkinase

&lt;300&gt;

&lt;308&gt; GenBank HSU09860

&lt;309&gt; 1995-06-03

&lt;400&gt; 63

accagacagt	tcttaaatta	gcaagccttc	aaaacccaaaa	atg	ggg	tcg	aaa	aga		55						
				Met	Gly	Ser	Lys	Arg								
				1				5								
ggc	ata	tct	tct	agg	cat	cat	tct	ctc	agc	tcc	tat	gaa	atc	atg	ttt	103
Gly	Ile	Ser	Ser	Arg	His	His	Ser	Leu	Ser	Ser	Tyr	Glu	Ile	Met	Phe	
				10					15					20		
gca	gct	ctc	ttt	gcc	ata	ttg	gta	gtg	ctc	tgt	gct	gga	tta	att	gca	151
Ala	Ala	Leu	Phe	Ala	Ile	Leu	Val	Val	Leu	Cys	Ala	Gly	Leu	Ile	Ala	
			25					30					35			
gta	tcc	tgc	ctg	aca	atc	aag	gaa	tcc	caa	cga	ggg	gca	gca	ctt	gga	199
Val	Ser	Cys	Leu	Thr	Ile	Lys	Glu	Ser	Gln	Arg	Gly	Ala	Ala	Leu	Gly	
		40					45					50				
cag	agt	cat	gaa	gcc	aga	gcg	aca	ttt	aaa	ata	aca	tcc	gga	gtt	aca	247
Gln	Ser	His	Glu	Ala	Arg	Ala	Thr	Phe	Lys	Ile	Thr	Ser	Gly	Val	Thr	
	55					60					65					
tat	aat	cct	aat	ttg	caa	gac	aaa	ctc	tca	gtg	gat	ttc	aaa	gtt	ctt	295
Tyr	Asn	Pro	Asn	Leu	Gln	Asp	Lys	Leu	Ser	Val	Asp	Phe	Lys	Val	Leu	
70					75				80						85	
gct	ttt	gac	ctt	cag	caa	atg	ata	gat	gag	atc	ttt	cta	tca	agc	aat	343
Ala	Phe	Asp	Leu	Gln	Gln	Met	Ile	Asp	Glu	Ile	Phe	Leu	Ser	Ser	Asn	
				90					95					100		
ctg	aag	aat	gaa	tat	aag	aac	tca	aga	ggt	tta	caa	ttt	gaa	aat	ggc	391
Leu	Lys	Asn	Glu	Tyr	Lys	Asn	Ser	Arg	Val	Leu	Gln	Phe	Glu	Asn	Gly	
			105					110					115			
agc	att	ata	gtc	gta	ttt	gac	ctt	ttc	ttt	gcc	cag	tgg	gtg	tca	gat	439
Ser	Ile	Ile	Val	Val	Phe	Asp	Leu	Phe	Phe	Ala	Gln	Trp	Val	Ser	Asp	
		120					125					130				
caa	aat	gta	aaa	gaa	gaa	ctg	att	caa	ggc	ctt	gaa	gca	aat	aaa	tcc	487
Gln	Asn	Val	Lys	Glu	Glu	Leu	Ile	Gln	Gly	Leu	Glu	Ala	Asn	Lys	Ser	
	135					140					145					
agc	caa	ctg	gtc	act	ttc	cat	att	gat	ttg	aac	agc	gtt	gat	atc	cta	535
Ser	Gln	Leu	Val	Thr	Phe	His	Ile	Asp	Leu	Asn	Ser	Val	Asp	Ile	Leu	
150					155				160					165		
gac	aag	cta	aca	acc	acc	agt	cat	ctg	gca	act	cca	gga	aat	gtc	tca	583
Asp	Lys	Leu	Thr	Thr	Thr	Ser	His	Leu	Ala	Thr	Pro	Gly	Asn	Val	Ser	
				170					175					180		
ata	gag	tgc	ctg	cct	ggg	tca	agt	cct	tgt	act	gat	gct	cta	acg	tgt	631
Ile	Glu	Cys	Leu	Pro	Gly	Ser	Ser	Pro	Cys	Thr	Asp	Ala	Leu	Thr	Cys	
			185					190					195			
ata	aaa	gct	gat	tta	ttt	tgt	gat	gga	gaa	gta	aac	tgt	cca	gat	ggg	679
Ile	Lys	Ala	Asp	Leu	Phe	Cys	Asp	Gly	Glu	Val	Asn	Cys	Pro	Asp	Gly	
		200					205					210				
tct	gac	gaa	gac	aat	aaa	atg	tgt	gcc	aca	ggt	tgt	gat	gga	aga	ttt	727

Ser	Asp	Glu	Asp	Asn	Lys	Met	Cys	Ala	Thr	Val	Cys	Asp	Gly	Arg	Phe		
215						220					225						
ttg	tta	act	gga	tca	tct	ggg	tct	ttc	cag	gct	act	cat	tat	cca	aaa	775	
Leu	Leu	Thr	Gly	Ser	Ser	Gly	Ser	Phe	Gln	Ala	Thr	His	Tyr	Pro	Lys		
230					235				240						245		
cct	tct	gaa	aca	agt	gtt	gtc	tgc	cag	tgg	atc	ata	cgt	gta	aac	caa	823	
Pro	Ser	Glu	Thr	Ser	Val	Val	Cys	Gln	Trp	Ile	Ile	Arg	Val	Asn	Gln		
				250					255					260			
gga	ctt	tcc	att	aaa	ctg	agc	ttc	gat	gat	ttt	aat	aca	tat	tat	aca	871	
Gly	Leu	Ser	Ile	Lys	Leu	Ser	Phe	Asp	Asp	Phe	Asn	Thr	Tyr	Tyr	Thr		
			265					270					275				
gat	ata	tta	gat	att	tat	gaa	ggg	gta	gga	tca	agc	aag	att	tta	aga	919	
Asp	Ile	Leu	Asp	Ile	Tyr	Glu	Gly	Val	Gly	Ser	Ser	Lys	Ile	Leu	Arg		
		280					285					290					
gct	tct	att	tgg	gaa	act	aat	cct	ggc	aca	ata	aga	att	ttt	tcc	aac	967	
Ala	Ser	Ile	Trp	Glu	Thr	Asn	Pro	Gly	Thr	Ile	Arg	Ile	Phe	Ser	Asn		
	295					300					305						
caa	gtt	act	gcc	acc	ttt	ctt	ata	gaa	tct	gat	gaa	agt	gat	tat	gtt	1015	
Gln	Val	Thr	Ala	Thr	Phe	Leu	Ile	Glu	Ser	Asp	Glu	Ser	Asp	Tyr	Val		
310					315					320					325		
ggc	ttt	aat	gca	aca	tat	act	gca	ttt	aac	agc	agt	gag	ctt	aat	aat	1063	
Gly	Phe	Asn	Ala	Thr	Tyr	Thr	Ala	Phe	Asn	Ser	Ser	Glu	Leu	Asn	Asn		
			330					335						340			
tat	gag	aaa	att	aat	tgt	aac	ttt	gag	gat	ggc	ttt	tgt	ttc	tgg	gtc	1111	
Tyr	Glu	Lys	Ile	Asn	Cys	Asn	Phe	Glu	Asp	Gly	Phe	Cys	Phe	Trp	Val		
		345						350					355				
cag	gat	cta	aat	gat	gat	aat	gaa	tgg	gaa	agg	att	cag	gga	agc	acc	1159	
Gln	Asp	Leu	Asn	Asp	Asp	Asn	Glu	Trp	Glu	Arg	Ile	Gln	Gly	Ser	Thr		
		360				365						370					
ttt	tct	cct	ttt	act	gga	ccc	aat	ttt	gac	cac	act	ttt	ggc	aat	gct	1207	
Phe	Ser	Pro	Phe	Thr	Gly	Pro	Asn	Phe	Asp	His	Thr	Phe	Gly	Asn	Ala		
	375				380					385							
tca	gga	ttt	tac	att	tct	acc	cca	act	gga	cca	gga	ggg	aga	caa	gaa	1255	
Ser	Gly	Phe	Tyr	Ile	Ser	Thr	Pro	Thr	Gly	Pro	Gly	Gly	Arg	Gln	Glu		
390					395				400						405		
cga	gtg	ggg	ctt	tta	agc	ctc	cct	ttg	gac	ccc	act	ttg	gag	cca	gct	1303	
Arg	Val	Gly	Leu	Leu	Ser	Leu	Pro	Leu	Asp	Pro	Thr	Leu	Glu	Pro	Ala		
			410					415						420			
tgc	ctt	agt	ttc	tgg	tat	cat	atg	tat	ggg	gaa	aat	gtc	cat	aaa	tta	1351	
Cys	Leu	Ser	Phe	Trp	Tyr	His	Met	Tyr	Gly	Glu	Asn	Val	His	Lys	Leu		
			425					430					435				
agc	att	aat	atc	agc	aat	gac	caa	aat	atg	gag	aag	aca	gtt	ttc	caa	1399	
Ser	Ile	Asn	Ile	Ser	Asn	Asp	Gln	Asn	Met	Glu	Lys	Thr	Val	Phe	Gln		
		440				445						450					
aag	gaa	gga	aat	tat	gga	gac	aat	tgg	aat	tat	gga	caa	gta	acc	cta	1447	
Lys	Glu	Gly	Asn	Tyr	Gly	Asp	Asn	Trp	Asn	Tyr	Gly	Gln	Val	Thr	Leu		
	455				460						465						

aat gaa aca gtt aaa ttt aag gtt gct ttt aat gct ttt aaa aac aag	1495
Asn Glu Thr Val Lys Phe Lys Val Ala Phe Asn Ala Phe Lys Asn Lys	
470 475 480 485	
atc ctg agt gat att gcg ttg gat gac att agc cta aca tat ggg att	1543
Ile Leu Ser Asp Ile Ala Leu Asp Asp Ile Ser Leu Thr Tyr Gly Ile	
490 495 500	
tgc aat ggg agt ctt tat cca gaa cca act ttg gtg cca act cct cca	1591
Cys Asn Gly Ser Leu Tyr Pro Glu Pro Thr Leu Val Pro Thr Pro Pro	
505 510 515	
cca gaa ctt cct acg gac tgt gga gga cct ttt gag ctg tgg gag cca	1639
Pro Glu Leu Pro Thr Asp Cys Gly Gly Pro Phe Glu Leu Trp Glu Pro	
520 525 530	
aat aca aca ttc agt tct acg aac ttt cca aac agc tac cct aat ctg	1687
Asn Thr Thr Phe Ser Ser Thr Asn Phe Pro Asn Ser Tyr Pro Asn Leu	
535 540 545	
gct ttc tgt gtt tgg att tta aat gca caa aaa gga aag aat ata caa	1735
Ala Phe Cys Val Trp Ile Leu Asn Ala Gln Lys Gly Lys Asn Ile Gln	
550 555 560 565	
ctt cat ttt caa gaa ttt gac tta gaa aat att aac gat gta gtt gaa	1783
Leu His Phe Gln Glu Phe Asp Leu Glu Asn Ile Asn Asp Val Val Glu	
570 575 580	
ata aga gat ggt gaa gaa gct gat tcc ttg ctc tta gct gtg tac aca	1831
Ile Arg Asp Gly Glu Glu Ala Asp Ser Leu Leu Leu Ala Val Tyr Thr	
585 590 595	
ggg cct ggc cca gta aag gat gtg ttc tct acc acc aac aga atg act	1879
Gly Pro Gly Pro Val Lys Asp Val Phe Ser Thr Thr Asn Arg Met Thr	
600 605 610	
gtg ctt ctc atc act aac gat gtg ttg gca aga gga ggg ttt aaa gca	1927
Val Leu Leu Ile Thr Asn Asp Val Leu Ala Arg Gly Gly Phe Lys Ala	
615 620 625	
aac ttt act act ggc tat cac ttg ggg att cca gag cca tgc aag gca	1975
Asn Phe Thr Thr Gly Tyr His Leu Gly Ile Pro Glu Pro Cys Lys Ala	
630 635 640 645	
gac cat ttt caa tgt aaa aat gga gag tgt gtt cca ctg gtg aat ctc	2023
Asp His Phe Gln Cys Lys Asn Gly Glu Cys Val Pro Leu Val Asn Leu	
650 655 660	
tgt gac ggt cat ctg cac tgt gag gat ggc tca gat gaa gca gat tgt	2071
Cys Asp Gly His Leu His Cys Glu Asp Gly Ser Asp Glu Ala Asp Cys	
665 670 675	
gtg cgt ttt ttc aat ggc aca acg aac aac aat ggt tta gtg cgg ttc	2119
Val Arg Phe Phe Asn Gly Thr Thr Asn Asn Asn Gly Leu Val Arg Phe	
680 685 690	
aga atc cag agc ata tgg cat aca gct tgt gct gag aac tgg acc acc	2167
Arg Ile Gln Ser Ile Trp His Thr Ala Cys Ala Glu Asn Trp Thr Thr	
695 700 705	
cag att tca aat gat gtt tgt caa ctg ctg gga cta ggg agt gga aac	2215

Gln	Ile	Ser	Asn	Asp	Val	Cys	Gln	Leu	Leu	Gly	Leu	Gly	Ser	Gly	Asn		
710					715					720					725		
tca	tca	aag	cca	atc	ttc	tct	acc	gat	ggc	gga	cca	ttt	gtc	aaa	tta	2263	
Ser	Ser	Lys	Pro	Ile	Phe	Ser	Thr	Asp	Gly	Gly	Pro	Phe	Val	Lys	Leu		
				730					735					740			
aac	aca	gca	cct	gat	ggc	cac	tta	ata	cta	aca	ccc	agt	caa	cag	tgt	2311	
Asn	Thr	Ala	Pro	Asp	Gly	His	Leu	Ile	Leu	Thr	Pro	Ser	Gln	Gln	Cys		
			745				750						755				
tta	cag	gat	tcc	ttg	att	cgg	tta	cag	tgt	aac	cat	aaa	tct	tgt	gga	2359	
Leu	Gln	Asp	Ser	Leu	Ile	Arg	Leu	Gln	Cys	Asn	His	Lys	Ser	Cys	Gly		
		760				765						770					
aaa	aaa	ctg	gca	gct	caa	gac	atc	acc	cca	aag	att	gtt	gga	gga	agt	2407	
Lys	Lys	Leu	Ala	Ala	Gln	Asp	Ile	Thr	Pro	Lys	Ile	Val	Gly	Gly	Ser		
	775					780					785						
aat	gcc	aaa	gaa	ggg	gcc	tgg	ccc	tgg	gtt	gtg	ggc	ctg	tat	tat	ggc	2455	
Asn	Ala	Lys	Glu	Gly	Ala	Trp	Pro	Trp	Val	Val	Gly	Leu	Tyr	Tyr	Gly		
	790				795				800						805		
ggc	cga	ctg	ctc	tgc	ggc	gca	tct	ctc	gtc	agc	agt	gac	tgg	ctg	gtg	2503	
Gly	Arg	Leu	Leu	Cys	Gly	Ala	Ser	Leu	Val	Ser	Ser	Asp	Trp	Leu	Val		
			810						815					820			
tcc	gcc	gca	cac	tgc	gtg	tat	ggg	aga	aac	tta	gag	cca	tcc	aag	tgg	2551	
Ser	Ala	Ala	His	Cys	Val	Tyr	Gly	Arg	Asn	Leu	Glu	Pro	Ser	Lys	Trp		
			825				830						835				
aca	gca	atc	cta	ggc	ctg	cat	atg	aaa	tca	aat	ctg	acc	tct	cct	caa	2599	
Thr	Ala	Ile	Leu	Gly	Leu	His	Met	Lys	Ser	Asn	Leu	Thr	Ser	Pro	Gln		
		840					845					850					
aca	gtc	cct	cga	tta	ata	gat	gaa	att	gtc	ata	aac	cct	cat	tac	aat	2647	
Thr	Val	Pro	Arg	Leu	Ile	Asp	Glu	Ile	Val	Ile	Asn	Pro	His	Tyr	Asn		
	855					860				865							
agg	cga	aga	aag	gac	aac	gac	att	gcc	atg	atg	cat	ctg	gaa	ttt	aaa	2695	
Arg	Arg	Arg	Lys	Asp	Asn	Asp	Ile	Ala	Met	Met	His	Leu	Glu	Phe	Lys		
	870				875				880					885			
gtg	aat	tac	aca	gat	tac	ata	caa	cct	att	tgt	tta	ccg	gaa	gaa	aat	2743	
Val	Asn	Tyr	Thr	Asp	Tyr	Ile	Gln	Pro	Ile	Cys	Leu	Pro	Glu	Glu	Asn		
				890				895						900			
caa	gtt	ttt	cct	cca	gga	aga	aat	tgt	tct	att	gct	ggc	tgg	ggg	acg	2791	
Gln	Val	Phe	Pro	Pro	Gly	Arg	Asn	Cys	Ser	Ile	Ala	Gly	Trp	Gly	Thr		
			905					910					915				
gtt	gta	tat	caa	ggc	act	act	gca	aac	ata	ttg	caa	gaa	gct	gat	gtt	2839	
Val	Val	Tyr	Gln	Gly	Thr	Thr	Ala	Asn	Ile	Leu	Gln	Glu	Ala	Asp	Val		
		920					925					930					
cct	ctt	cta	tca	aat	gag	aga	tgc	caa	cag	cag	atg	cca	gaa	tat	aac	2887	
Pro	Leu	Leu	Ser	Asn	Glu	Arg	Cys	Gln	Gln	Gln	Met	Pro	Glu	Tyr	Asn		
	935					940					945						
att	act	gaa	aat	atg	ata	tgt	gca	ggc	tat	gaa	gaa	gga	gga	ata	gat	2935	
Ile	Thr	Glu	Asn	Met	Ile	Cys	Ala	Gly	Tyr	Glu	Glu	Gly	Gly	Ile	Asp		
					955					960					965		

tct tgt cag ggg gat tca gga gga cca tta atg tgc caa gaa aac aac 2983  
 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Glu Asn Asn  
                   970                                  975                                  980

agg tgg ttc ctt gct ggt gtg acc tca ttt gga tac aag tgt gcc ctg 3031  
 Arg Trp Phe Leu Ala Gly Val Thr Ser Phe Gly Tyr Lys Cys Ala Leu  
                   985                                  990                                  995

cct aat cgc ccc gga gtg tat gcc agg gtc tca agg ttt acc gaa tgg 3079  
 Pro Asn Arg Pro Gly Val Tyr Ala Arg Val Ser Arg Phe Thr Glu Trp  
                   1000                                  1005                                  1010

ata caa agt ttt cta cat tag cgcatttctt aaactaaaca ggaaagtgcg 3130  
 Ile Gln Ser Phe Leu His \*  
                   1015

attattttcc cattctactc tagaaagcat ggaaattaag tgtttcgtac aaaaatttta 3190  
 aaaagttacc aaaggttttt attcttacct atgtcaatga aatgctaggg ggccagggaa 3250  
 acaaaaatttt aaaaataata aaattcacca tagcaataga gaataacttt aaaataccat 3310  
 taaatacatt tgtatttcat tgtgaacagg tatttcttca cagatctcat ttttaaaatt 3370  
 cttaatgatt atttttatta cttactgttg tttaaaggga tgttatttta aagcatatac 3430  
 catacactta agaaatttga gcagaattta aaaaagaaag aaaataaatt gtttttccca 3490  
 aagtatgtca ctgttggaag taaactgcca taaattttct agttccagtt tagtttgctg 3550  
 ctatttagcag aaactcaatt gtttctctgt cttttctatc aaaattttca acatatgcat 3610  
 aaccttagta ttttcccaac caatagaaac tattttattgt aagcttatgt cacaggcctg 3670  
 gactaaattg attttacgtt cctctt 3696

<210> 64  
 <211> 1019  
 <212> PRT  
 <213> Homo Sapien

<400> 64  
 Met Gly Ser Lys Arg Gly Ile Ser Ser Arg His His Ser Leu Ser Ser  
   1                  5                  10                                  15  
 Tyr Glu Ile Met Phe Ala Ala Leu Phe Ala Ile Leu Val Val Leu Cys  
                   20                  25                                  30  
 Ala Gly Leu Ile Ala Val Ser Cys Leu Thr Ile Lys Glu Ser Gln Arg  
                   35                  40                                  45  
 Gly Ala Ala Leu Gly Gln Ser His Glu Ala Arg Ala Thr Phe Lys Ile  
   50                  55                  60  
 Thr Ser Gly Val Thr Tyr Asn Pro Asn Leu Gln Asp Lys Leu Ser Val  
   65                  70                  75                                  80  
 Asp Phe Lys Val Leu Ala Phe Asp Leu Gln Gln Met Ile Asp Glu Ile  
                   85                  90                                  95  
 Phe Leu Ser Ser Asn Leu Lys Asn Glu Tyr Lys Asn Ser Arg Val Leu  
                   100                  105                                  110  
 Gln Phe Glu Asn Gly Ser Ile Ile Val Val Phe Asp Leu Phe Phe Ala  
                   115                  120                                  125  
 Gln Trp Val Ser Asp Gln Asn Val Lys Glu Glu Leu Ile Gln Gly Leu  
   130                  135                  140  
 Glu Ala Asn Lys Ser Ser Gln Leu Val Thr Phe His Ile Asp Leu Asn  
   145                  150                  155                                  160  
 Ser Val Asp Ile Leu Asp Lys Leu Thr Thr Ser His Leu Ala Thr  
                   165                  170                                  175  
 Pro Gly Asn Val Ser Ile Glu Cys Leu Pro Gly Ser Ser Pro Cys Thr  
                   180                  185                                  190  
 Asp Ala Leu Thr Cys Ile Lys Ala Asp Leu Phe Cys Asp Gly Glu Val  
                   195                  200                                  205  
 Asn Cys Pro Asp Gly Ser Asp Glu Asp Asn Lys Met Cys Ala Thr Val  
                   210                  215                                  220

Cys	Asp	Gly	Arg	Phe	Leu	Leu	Thr	Gly	Ser	Ser	Gly	Ser	Phe	Gln	Ala
225					230					235					240
Thr	His	Tyr	Pro	Lys	Pro	Ser	Glu	Thr	Ser	Val	Val	Cys	Gln	Trp	Ile
				245					250					255	
Ile	Arg	Val	Asn	Gln	Gly	Leu	Ser	Ile	Lys	Leu	Ser	Phe	Asp	Asp	Phe
			260					265					270		
Asn	Thr	Tyr	Tyr	Thr	Asp	Ile	Leu	Asp	Ile	Tyr	Glu	Gly	Val	Gly	Ser
		275				280						285			
Ser	Lys	Ile	Leu	Arg	Ala	Ser	Ile	Trp	Glu	Thr	Asn	Pro	Gly	Thr	Ile
	290					295					300				
Arg	Ile	Phe	Ser	Asn	Gln	Val	Thr	Ala	Thr	Phe	Leu	Ile	Glu	Ser	Asp
305				310						315					320
Glu	Ser	Asp	Tyr	Val	Gly	Phe	Asn	Ala	Thr	Tyr	Thr	Ala	Phe	Asn	Ser
				325					330					335	
Ser	Glu	Leu	Asn	Asn	Tyr	Glu	Lys	Ile	Asn	Cys	Asn	Phe	Glu	Asp	Gly
			340					345					350		
Phe	Cys	Phe	Trp	Val	Gln	Asp	Leu	Asn	Asp	Asp	Asn	Glu	Trp	Glu	Arg
		355					360					365			
Ile	Gln	Gly	Ser	Thr	Phe	Ser	Pro	Phe	Thr	Gly	Pro	Asn	Phe	Asp	His
	370					375					380				
Thr	Phe	Gly	Asn	Ala	Ser	Gly	Phe	Tyr	Ile	Ser	Thr	Pro	Thr	Gly	Pro
385				390						395					400
Gly	Gly	Arg	Gln	Glu	Arg	Val	Gly	Leu	Leu	Ser	Leu	Pro	Leu	Asp	Pro
				405					410					415	
Thr	Leu	Glu	Pro	Ala	Cys	Leu	Ser	Phe	Trp	Tyr	His	Met	Tyr	Gly	Glu
			420					425					430		
Asn	Val	His	Lys	Leu	Ser	Ile	Asn	Ile	Ser	Asn	Asp	Gln	Asn	Met	Glu
		435					440					445			
Lys	Thr	Val	Phe	Gln	Lys	Glu	Gly	Asn	Tyr	Gly	Asp	Asn	Trp	Asn	Tyr
	450					455					460				
Gly	Gln	Val	Thr	Leu	Asn	Glu	Thr	Val	Lys	Phe	Lys	Val	Ala	Phe	Asn
465					470					475					480
Ala	Phe	Lys	Asn	Lys	Ile	Leu	Ser	Asp	Ile	Ala	Leu	Asp	Asp	Ile	Ser
				485					490					495	
Leu	Thr	Tyr	Gly	Ile	Cys	Asn	Gly	Ser	Leu	Tyr	Pro	Glu	Pro	Thr	Leu
			500					505					510		
Val	Pro	Thr	Pro	Pro	Pro	Glu	Leu	Pro	Thr	Asp	Cys	Gly	Gly	Pro	Phe
		515					520					525			
Glu	Leu	Trp	Glu	Pro	Asn	Thr	Thr	Phe	Ser	Ser	Thr	Asn	Phe	Pro	Asn
		530				535					540				
Ser	Tyr	Pro	Asn	Leu	Ala	Phe	Cys	Val	Trp	Ile	Leu	Asn	Ala	Gln	Lys
545					550					555					560
Gly	Lys	Asn	Ile	Gln	Leu	His	Phe	Gln	Glu	Phe	Asp	Leu	Glu	Asn	Ile
				565					570					575	
Asn	Asp	Val	Val	Glu	Ile	Arg	Asp	Gly	Glu	Glu	Ala	Asp	Ser	Leu	Leu
			580					585					590		
Leu	Ala	Val	Tyr	Thr	Gly	Pro	Gly	Pro	Val	Lys	Asp	Val	Phe	Ser	Thr
		595					600					605			
Thr	Asn	Arg	Met	Thr	Val	Leu	Leu	Ile	Thr	Asn	Asp	Val	Leu	Ala	Arg
		610				615					620				
Gly	Gly	Phe	Lys	Ala	Asn	Phe	Thr	Thr	Gly	Tyr	His	Leu	Gly	Ile	Pro
625					630					635					640
Glu	Pro	Cys	Lys	Ala	Asp	His	Phe	Gln	Cys	Lys	Asn	Gly	Glu	Cys	Val
				645					650					655	
Pro	Leu	Val	Asn	Leu	Cys	Asp	Gly	His	Leu	His	Cys	Glu	Asp	Gly	Ser
			660					665					670		
Asp	Glu	Ala	Asp	Cys	Val	Arg	Phe	Phe	Asn	Gly	Thr	Thr	Asn	Asn	Asn
		675					680					685			
Gly	Leu	Val	Arg	Phe	Arg	Ile	Gln	Ser	Ile	Trp	His	Thr	Ala	Cys	Ala
	690					695					700				
Glu	Asn	Trp	Thr	Thr	Gln	Ile	Ser	Asn	Asp	Val	Cys	Gln	Leu	Leu	Gly
705					710					715					720

```
<210> 65
<211> 1500
<212> DNA
<213> Homo Sapien
```

<300>  
<308> GenBank AB002134  
<309> 1998-06-04

tat gta gta tgt ttc att gtc gtc gca ggg gta gtg atc ctg gca gtc 157  
Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val

20										25										30										
acc	ata	gct	cta	ctt	gtt	tac	ttt	tta	gct	ttt	gat	caa	aaa	tct	tac	205														
Thr	Ile	Ala	Leu	Leu	Val	Tyr	Phe	Leu	Ala	Phe	Asp	Gln	Lys	Ser	Tyr															
		35					40					45																		
ttt	tat	agg	agc	agt	ttt	caa	ctc	cta	aat	gtt	gaa	tat	aat	agt	cag	253														
Phe	Tyr	Arg	Ser	Ser	Phe	Gln	Leu	Leu	Asn	Val	Glu	Tyr	Asn	Ser	Gln															
	50					55					60																			
tta	aat	tca	cca	gct	aca	cag	gaa	tac	agg	act	ttg	agt	gga	aga	att	301														
Leu	Asn	Ser	Pro	Ala	Thr	Gln	Glu	Tyr	Arg	Thr	Leu	Ser	Gly	Arg	Ile															
	65				70				75						80															
gaa	tct	ctg	att	act	aaa	aca	ttc	aaa	gaa	tca	aat	tta	aga	aat	cag	349														
Glu	Ser	Leu	Ile	Thr	Lys	Thr	Phe	Lys	Glu	Ser	Asn	Leu	Arg	Asn	Gln															
				85					90					95																
ttc	atc	aga	gct	cat	gtt	gcc	aaa	ctg	agg	caa	gat	ggg	agt	ggg	gtg	397														
Phe	Ile	Arg	Ala	His	Val	Ala	Lys	Leu	Arg	Gln	Asp	Gly	Ser	Gly	Val															
			100					105					110																	
aga	gcg	gat	gtt	gtc	atg	aaa	ttt	caa	ttc	act	aga	aat	aac	aat	gga	445														
Arg	Ala	Asp	Val	Val	Met	Lys	Phe	Gln	Phe	Thr	Arg	Asn	Asn	Asn	Gly															
		115					120					125																		
gca	tca	atg	aaa	agc	aga	att	gag	tct	gtt	tta	cga	caa	atg	ctg	aat	493														
Ala	Ser	Met	Lys	Ser	Arg	Ile	Glu	Ser	Val	Leu	Arg	Gln	Met	Leu	Asn															
	130					135					140																			
aac	tct	gga	aac	ctg	gaa	ata	aac	cct	tca	act	gag	ata	aca	tca	ctt	541														
Asn	Ser	Gly	Asn	Leu	Glu	Ile	Asn	Pro	Ser	Thr	Glu	Ile	Thr	Ser	Leu															
	145				150				155						160															
act	gac	cag	gct	gca	gca	aat	tgg	ctt	att	aat	gaa	tgt	ggg	gcc	ggg	589														
Thr	Asp	Gln	Ala	Ala	Ala	Asn	Trp	Leu	Ile	Asn	Glu	Cys	Gly	Ala	Gly															
				165				170						175																
cca	gac	cta	ata	aca	ttg	tct	gag	cag	aga	atc	ctt	gga	ggc	act	gag	637														
Pro	Asp	Leu	Ile	Thr	Leu	Ser	Glu	Gln	Arg	Ile	Leu	Gly	Gly	Thr	Glu															
			180					185					190																	
gct	gag	gag	gga	agc	tgg	ccg	tgg	caa	gtc	agt	ctg	cgg	ctc	aat	aat	685														
Ala	Glu	Glu	Gly	Ser	Trp	Pro	Trp	Gln	Val	Ser	Leu	Arg	Leu	Asn	Asn															
		195					200					205																		
gcc	cac	cac	tgt	gga	ggc	agc	ctg	atc	aat	aac	atg	tgg	atc	ctg	aca	733														
Ala	His	His	Cys	Gly	Gly	Ser	Leu	Ile	Asn	Asn	Met	Trp	Ile	Leu	Thr															
	210					215					220																			
gca	gct	cac	tgc	ttc	aga	agc	aac	tct	aat	cct	cgt	gac	tgg	att	gcc	781														
Ala	Ala	His	Cys	Phe	Arg	Ser	Asn	Ser	Asn	Pro	Arg	Asp	Trp	Ile	Ala															
	225				230					235					240															
acg	tct	ggg	att	tcc	aca	aca	ttt	cct	aaa	cta	aga	atg	aga	gta	aga	829														
Thr	Ser	Gly	Ile	Ser	Thr	Thr	Phe	Pro	Lys	Leu	Arg	Met	Arg	Val	Arg															
				245					250					255																
aat	att	tta	att	cat	aac	aat	tat	aaa	tct	gca	act	cat	gaa	aat	gac	877														
Asn	Ile	Leu	Ile	His	Asn	Asn	Tyr	Lys	Ser	Ala	Thr	His	Glu	Asn	Asp															
			260					265					270																	

att gca ctt gtg aga ctt gag aac agt gtc acc ttt acc aaa gat atc 925  
 Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile  
 275 280 285

cat agt gtg tgt ctc cca gct gct acc cag aat att cca cct ggc tct 973  
 His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser  
 290 295 300

act gct tat gta aca gga tgg ggc gct caa gaa tat gct ggc cac aca 1021  
 Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr  
 305 310 315 320

gtt cca gag cta agg caa gga cag gtc aga ata ata agt aat gat gta 1069  
 Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val  
 325 330 335

tgt aat gca cca cat agt tat aat gga gcc atc ttg tct gga atg ctg 1117  
 Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu  
 340 345 350

tgt gct gga gta cct caa ggt gga gtg gac gca tgt cag ggt gac tct 1165  
 Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser  
 355 360 365

ggt ggc cca cta gta caa gaa gac tca cgg cgg ctt tgg ttt att gtg 1213  
 Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val  
 370 375 380

ggg ata gta agc tgg gga gat cag tgt ggc ctg ccg gat aag cca gga 1261  
 Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly  
 385 390 395 400

gtg tat act cga gtg aca gcc tac ctt gac tgg att agg caa caa act 1309  
 Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr  
 405 410 415

ggg atc tag tgcaacaagt gcattcctgt tgcaaaagtct gtatgcaggt 1358  
 Gly Ile \*

gtgcctgtct taaattccaa agctttacat ttcaactgaa aaagaaacta gaaatgtcct 1418  
 aatttaacat cttgttacat aaatatgggt taacaaacac tgtttaacct ttctttatta 1478  
 ttaaagggtt tctattttct cc 1500

<210> 66  
 <211> 418  
 <212> PRT  
 <213> Homo Sapien

<400> 66  
 Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro  
 1 5 10 15  
 Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val  
 20 25 30  
 Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr  
 35 40 45  
 Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln  
 50 55 60  
 Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile  
 65 70 75 80  
 Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln  
 85 90 95

Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val  
 100 105 110  
 Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly  
 115 120 125  
 Ala Ser Met Lys Ser Arg Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu  
 130 135 140 160  
 Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu  
 145 150 155 160  
 Thr Asp Gln Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly  
 165 170 175  
 Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu  
 180 185 190  
 Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn  
 195 200 205  
 Ala His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr  
 210 215 220  
 Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala  
 225 230 235 240  
 Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg  
 245 250 255  
 Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp  
 260 265 270  
 Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile  
 275 280 285  
 His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser  
 290 295 300  
 Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr  
 305 310 315 320  
 Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val  
 325 330 335  
 Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu  
 340 345 350  
 Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser  
 355 360 365  
 Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val  
 370 375 380  
 Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly  
 385 390 395 400  
 Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr  
 405 410 415  
 Gly Ile

<210> 67  
 <211> 1783  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> CDS  
 <222> (246)...(1499)  
 <223> Nucleotide sequence encoding human hepsin

<300>  
 <308> GenBank M18930  
 <309> 1993-06-11

<400> 67  
 tcgagccgc tttccaggga ccctacctga gggccacag gtgaggcagc ctggcctagc 60  
 aggccccacg ccaccgcctc tgcctccagg ccgcccgtg ctgcggggcc accatgctcc 120  
 tgcccaggcc tggagactga cccgaccccg gcactacctc gaggtccgc cccacactgc 180  
 tggacccag ggtcccaccc tggcccagga ggctagccag ggaatcatta acaagaggca 240

gtgac atg gcg cag aag gag ggt ggc cgg act gtg cca tgc tgc tcc aga	290
Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg	
1 5 10 15	
ccc aag gtg gca gct ctc act gcg ggg acc ctg cta ctt ctg aca gcc	338
Pro Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Thr Ala	
20 25 30	
atc ggg gcg gca tcc tgg gcc att gtg gct gtt ctc ctc agg agt gac	386
Ile Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp	
35 40 45	
cag gag ccg ctg tac cca gtg cag gtc agc tct gcg gac gct cgg ctc	434
Gln Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu	
50 55 60	
atg gtc ttt gac aag acg gaa ggg acg tgg cgg ctg ctg tgc tcc tcg	482
Met Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser	
65 70 75	
cgc tcc aac gcc agg gta gcc gga ctc agc tgc gag gag atg ggc ttc	530
Arg Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe	
80 85 90 95	
ctc agg gca ctg acc cac tcc gag ctg gac gtg cga acg gcg ggc gcc	578
Leu Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala	
100 105 110	
aat ggc acg tcg ggc ttc ttc tgt gtg gac gag ggg agg ctg ccc cac	626
Asn Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His	
115 120 125	
acc cag agg ctg ctg gag gtc atc tcc gtg tgt gat tgc ccc aga ggc	674
Thr Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly	
130 135 140	
cgt ttc ttg gcc gcc atc tgc caa gac tgt ggc cgc agg aag ctg ccc	722
Arg Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro	
145 150 155	
gtg gac cgc atc gtg gga ggc cgg gac acc agc ttg ggc cgg tgg ccg	770
Val Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro	
160 165 170 175	
tgg caa gtc agc ctt cgc tat gat gga gca cac ctc tgt ggg gga tcc	818
Trp Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser	
180 185 190	
ctg ctc tcc ggg gac tgg gtg ctg aca gcc gcc cac tgc ttc ccg gag	866
Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu	
195 200 205	
cgg aac cgg gtc ctg tcc cga tgg cga gtg ttt gcc ggt gcc gtg gcc	914
Arg Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala	
210 215 220	
cag gcc tct ccc cac ggt ctg cag ctg ggg gtg cag gct gtg gtc tac	962
Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr	
225 230 235	
cac ggg ggc tat ctt ccc ttt cgg gac ccc aac agc gag gag aac agc	1010
His Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser	

<400> 68  
Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg Pro  
1 5 10 15  
Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala Ile  
20 25 30

```

Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp Gln
      35              40              45
Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu Met
      50              55              60
Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser Arg
      65              70              75              80
Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe Leu
      85              90              95
Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala Asn
      100             105             110
Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His Thr
      115             120             125
Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly Arg
      130             135             140
Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro Val
      145             150             155             160
Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp
      165             170             175
Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser Leu
      180             185             190
Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg
      195             200             205
Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln
      210             215             220
Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His
      225             230             235             240
Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
      245             250             255
Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu Tyr
      260             265             270
Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp Gly
      275             280             285
Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly Gln
      290             295             300
Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn Asp
      305             310             315             320
Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met
      325             330             335
Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp
      340             345             350
Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg
      355             360             365
Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala
      370             375             380
Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile
      385             390             395             400
Phe Gln Ala Ile Lys Thr His Ser Glu Ala Ser Gly Met Val Thr Gln
      405             410             415
Leu

```

```

<210> 69
<211> 2479
<212> DNA
<213> Homo sapien

```

```

<220>
<221> CDS
<222> (57)...(1535)
<223> Nucleotide sequence encoding human serine protease

```

```

<300>

```

&lt;308&gt; GenBank U75329

&lt;309&gt; 1997-10-10

&lt;400&gt; 69

```

gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaag atg      59
                                                    Met
                                                    1

gct ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac      107
Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn
                    5                                10                    15

cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc      155
His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
                    20                                25                    30

ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg      203
Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val
                    35                                40                    45

ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc      251
Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
                    50                                55                                60                    65

tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act      299
Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
                    70                                75                                80

aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga      347
Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
                    85                                90                                95

gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc      395
Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys
                    100                                105                                110

tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc      443
Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro
                    115                                120                                125

tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag      491
Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu
                    130                                135                                140                    145

aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac      539
Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met Tyr
                    150                                155                                160

tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac      587
Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn
                    165                                170                                175

gag aac tac ggg ccg gcg gcc tgc agg gac atg ggc tat aag aat aat      635
Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn
                    180                                185                                190

ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt      683
Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe
                    195                                200                                205

atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg      731
Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu

```

210	215	220	225	
tac cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt				779
Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys	230	235	240	
tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg				827
Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val	245	250	255	
ggc ggt gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg				875
Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu	260	265	270	
cac gtc cag aac gtc cac gtg tgc gga gcc tcc atc atc acc ccc gag				923
His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu	275	280	285	
tgg atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca				971
Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro	290	295	300	305
tgg cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc				1019
Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe	310	315	320	
tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat				1067
Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn Tyr	325	330	335	
gac tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag				1115
Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys	340	345	350	
cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca				1163
Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro	355	360	365	
ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg				1211
Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly	370	375	380	385
gcc acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag				1259
Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys	390	395	400	
gtg ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac				1307
Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp	405	410	415	
aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac				1355
Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn	420	425	430	
gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aac				1403
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Asn	435	440	445	
aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt				1451
Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys	450	455	460	465

gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg 1499  
Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr  
470 475 480

gac tgg att tat cga caa atg aag gca aac ggc taa tccacatggg 1545  
Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly \*  
485 490

cttcgtcctt gacgtcgttt tacaagaaaa caatggggct ggttttgctt ccccgatgcat 1605  
gattttactct tagagatgat tcagagggtca cttcattttt attaaacagt gaacttgtct 1665  
ggcttttgcca ctctctgcca tactgtgcag gctgcagtgg cttccctgcc cagcctgctc 1725  
tccctaaccct cttgtccgca aggggtgatg gccggctggt tgtgggcact ggcgggtcaat 1785  
tgtggaagga agaggggttg aggtgcccc cattgagatc ttcctgctga gtcctttcca 1845  
ggggccaatt ttggatgagc atggagctgt cactttctcag ctgctggatg acttgagatg 1905  
aaaaaggaga gacatggaaa gggagacagc caggtggcac ctgcagcggc tgccctctgg 1965  
ggccacttgg tagtgtcccc agcctacttc acaaggggat tttgctgatg ggttcttaga 2025  
gccttagcag ccctggatgg tggccagaaa taaagggacc agcccttcat ggggtggtgac 2085  
gtggtagtca cttgtaaggg gaacagaaaac atttttgttc ttatgggggtg agaatataga 2145  
cagtgcctctt ggtgcgaggg aagcaattga aaaggaactt gccctgagca ctccctgtgc 2205  
aggtctccac ctgcacattg ggtggggctc ctgggagggg gactcagcct tcctcctcat 2265  
cctcctgac cctgctccta gcaccctgga gagtgaatgc cccttggtcc ctggcagggc 2325  
gccaagtttg gcacatgtc ggcctcttca ggcctgatag tcattggaaa ttgaggtcca 2385  
tgggggaaat caaggatgct cagttaaagg tacactgttt ccatgttatg tttctacaca 2445  
ttgatgggtg tgaccctgag ttcaaagcca tctt 2479

<210> 70  
<211> 492  
<212> PRT  
<213> Homo sapien

<400> 70  
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu  
1 5 10 15  
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val  
20 25 30  
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro  
35 40 45  
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val  
50 55 60  
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys  
65 70 75 80  
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val  
85 90 95  
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys  
100 105 110  
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn  
115 120 125  
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp  
130 135 140  
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met  
145 150 155  
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp  
165 170 175  
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn  
180 185 190  
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser  
195 200 205  
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys  
210 215 220  
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg  
225 230 235 240  
Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile

Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser  
 245 250 255  
 260 265 270  
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Thr Pro  
 275 280 285  
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn  
 290 295 300  
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met  
 305 310 315 320  
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn  
 325 330 335  
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln  
 340 345 350  
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn  
 355 360 365  
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp  
 370 375 380  
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala  
 385 390 395 400  
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr  
 405 410 415  
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly  
 420 425 430  
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser  
 435 440 445  
 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly  
 450 455 460  
 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe  
 465 470 475 480  
 Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly  
 485 490

<210> 71  
 <211> 2079  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> CDS  
 <222> (251)...(1522)  
 <223> Nucleotide sequence encoding transmembrane  
 protease, serine 4 (TMPRSS4)

<300>  
 <308> GenBank NM016425  
 <309> 2000-11-06

<400> 71  
 gagagggcagc agcttggttca gcggacaagg atgctggggcg tgagggacca aggcctgccc 60  
 tgcactcggg cctcctccag ccagtgctga ccagggactt ctgacctgct ggccagccag 120  
 gacctgtgtg gggaggccct cctgctgctt tggggtgaca atctcagctc caggctacag 180  
 ggagaccggg aggatcacag agccagcatg gtacaggatc ctgacagtga tcaacctctg 240  
 aacagcctcg atg tca aac ccc tgc gca aac ccc gta tcc cca tgg aga 289  
 Met Ser Asn Pro Cys Ala Asn Pro Val Ser Pro Trp Arg  
 1 5 10  
 cct tca gaa agt gtg ggg atc ccc atc atc ata gca cta ctg agc ctg 337  
 Pro Ser Glu Ser Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu  
 15 20 25  
 gcg agt atc atc att gtg gtt gtc ctc atc aag gtg att ctg gat aaa 385  
 Ala Ser Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys

30	35	40	45	
tac tac ttc ctc tgc ggg cag cct ctc cac ttc atc ccg agg aag cag				433
Tyr Tyr Phe Leu Cys 50	Gly Gln Pro Leu His 55	Phe Ile Pro Arg Lys 60	Gln	
ctg tgt gac gga gag ctg gac tgt ccc ttg ggg gag gac gag gag cac				481
Leu Cys Asp Gly 65	Glu Leu Asp Cys Pro 70	Gly Glu Asp Glu Glu His 75		
tgt gtc aag agc ttc ccc gaa ggg cct gca gtg gca gtc cgc ctc tcc				529
Cys Val Lys 80	Ser Phe Pro Glu Gly 85	Pro Ala Val Ala Val Arg Leu Ser 90		
aag gac cga tcc aca ctg cag gtg ctg gac tgc gcc aca ggg aac tgg				577
Lys Asp 95	Arg Ser Thr Leu Gln Val Leu Asp 100	Ser Ala Thr Gly Asn Trp 105		
ttc tct gcc tgt ttc gac aac ttc aca gaa gct ctc gct gag aca gcc				625
Phe Ser Ala Cys Phe 110	Asp Asn Phe Thr Glu Ala 115	Leu Ala Glu Thr Ala 120	125	
tgt agg cag atg ggc tac agc agc aaa ccc act ttc aga gct gtg gag				673
Cys Arg Gln Met 130	Gly Tyr Ser Ser Lys 135	Thr Phe Arg Ala Val Glu 140		
att ggc cca gac cag gat ctg gat gtt gtt gaa atc aca gaa aac agc				721
Ile Gly Pro 145	Asp Gln Asp Leu Asp Val 150	Glu Ile Thr Glu Asn Ser 155		
cag gag ctt cgc atg cgg aac tca agt ggg ccc tgt ctc tca ggc tcc				769
Gln Glu 160	Leu Arg Met Arg Asn Ser Ser Gly Pro Cys 165	Leu Ser Gly Ser 170		
ctg gtc tcc ctg cac tgt ctt gcc tgt ggg aag agc ctg aag acc ccc				817
Leu Val Ser Leu His 175	Cys Leu Ala Cys Gly Lys 180	Ser Leu Lys Thr Pro 185		
cgt gtg gtg ggt ggg gag gag gcc tct gtg gat tct tgg cct tgg cag				865
Arg Val Val Gly 190	Gly Glu Glu Ala Ser Val Asp 195	Ser Trp Pro Trp Glu 200	205	
gtc agc atc cag tac gac aaa cag cac gtc tgt gga ggg agc atc ctg				913
Val Ser Ile Gln Tyr 210	Asp Lys Gln His Val Cys 215	Gly Gly Ser Ile Leu 220		
gac ccc cac tgg gtc ctc acg gca gcc cac tgc ttc agg aaa cat acc				961
Asp Pro His Trp 225	Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr 230	235		
gat gtg ttc aac tgg aag gtg cgg gca ggc tca gac aaa ctg ggc agc				1009
Asp Val Phe Asn Trp 240	Lys Val Arg Ala Gly Ser Asp Lys 245	Leu Gly Ser 250		
ttc cca tcc ctg gct gtg gcc aag atc atc atc att gaa ttc aac ccc				1057
Phe Pro Ser Leu Ala Val 255	Ala Lys Ile Ile Ile 260	Ile Glu Phe Asn Pro 265		
atg tac ccc aaa gac aat gac atc gcc ctc atg aag ctg cag ttc cca				1105
Met Tyr Pro Lys Asp 270	Asn Asp Ile Ala Leu Met 275	Lys Leu Gln Phe Pro 280	285	

ctc act ttc tca ggc aca gtc agg ccc atc tgt ctg ccc ttc ttt gat 1153  
 Leu Thr Phe Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp  
 290 295 300

gag gag ctc act cca gcc acc cca ctc tgg atc att gga tgg ggc ttt 1201  
 Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe  
 305 310 315

acg aag cag aat gga ggg aag atg tct gac ata ctg ctg cag gcg tca 1249  
 Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser  
 320 325 330

gtc cag gtc att gac agc aca cgg tgc aat gca gac gat gcg tac cag 1297  
 Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln  
 335 340 345

ggg gaa gtc acc gag aag atg atg tgt gca ggc atc ccg gaa ggg ggt 1345  
 Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly  
 350 355 360 365

gtg gac acc tgc cag ggt gac agt ggt ggg ccc ctg atg tac caa tct 1393  
 Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser  
 370 375 380

gac cag tgg cat gtg gtg ggc atc gtt agc tgg ggc tat ggc tgc ggg 1441  
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly  
 385 390 395

ggc ccg agc acc cca gga gta tac acc aag gtc tca gcc tat ctc aac 1489  
 Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn  
 400 405 410

tgg atc tac aat gtc tgg aag gct gag ctg taa tgctgctgcc cctttgcagt 1542  
 Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu \*  
 415 420

gctgggagcc gcttccttcc tgccctgccc acctggggat cccccaaagt cagacacaga 1602  
 gcaagagtc ccttgggtac acccctctgc ccacagcctc agcatttctt ggagcagcaa 1662  
 agggcctcaa ttctgtgaag agaccctcgc agcccagagg cgcccagagg aagtcagcag 1722  
 ccctagctcg gccacacttg gtgctcccag catcccaggg agagacacag cccactgaac 1782  
 aaggtctcag gggatttgc t aagccaagaa ggaactttcc cacactactg aatggaagca 1842  
 ggctgtcttg taaaagccca gatcactgtg ggctggagag gagaaggaaa gggctctgcgc 1902  
 cagccctgtc cgtcttcacc catccccaag cctactagag caagaaacca gttgtaatat 1962  
 aaaatgcact gccctactgt tggatatgact accgttacct actgttgtca ttgttattac 2022  
 agctatggcc actattatta aagagctgtg taacatcaaa aaaaaaaaaa aaaaaaa 2079

<210> 72  
 <211> 423  
 <212> PRT  
 <213> Homo sapien

<400> 72  
 Met Ser Asn Pro Cys Ala Asn Pro Val Ser Pro Trp Arg Pro Ser Glu  
 1 5 10 15  
 Ser Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile  
 20 25 30  
 Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe  
 35 40 45  
 Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp  
 50 55 60  
 Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys  
 65 70 75 80

Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg  
 85 90 95  
 Ser Thr Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala  
 100 105 110  
 Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln  
 115 120 125  
 Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro  
 130 135 140  
 Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu  
 145 150 155 160  
 Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser  
 165 170 175  
 Leu His Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val  
 180 185 190  
 Gly Gly Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile  
 195 200 205  
 Gln Tyr Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His  
 210 215 220  
 Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe  
 225 230 235 240  
 Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser  
 245 250 255  
 Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro  
 260 265 270  
 Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe  
 275 280 285  
 Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu  
 290 295 300  
 Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln  
 305 310 315 320  
 Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val  
 325 330 335  
 Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val  
 340 345 350  
 Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr  
 355 360 365  
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp  
 370 375 380  
 His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser  
 385 390 395 400  
 Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr  
 405 410 415  
 Asn Val Trp Lys Ala Glu Leu  
 420